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May 29, 2003, 08:39:22 ; Search time 49 Seconds (without alignments) 2056.099 Million cell updates/sec
                                                                                                                                                                                      US-10-031-146-2
1048
1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            283224 seqs, 96134422 residues
                                                                           OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                          Title:
Perfect score:
Sequence:
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Post-processing: Listing first 45 summaries

283224

Total number of hits satisfying chosen parameters:

0

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	NADPH-ferrihemopro	NADPH-ferrihemopro	cytochrome P450 /	nadph-cytochrome p	NADPH-ferrihemopro	NADPH-ferrihemopro	probable NADPH cyt	sulfite reductase	sulfite reductase	NADPH-ferrihemopro	probable FAD bindi	NADPH-ferrihemopro	NADPH-ferrihemopro	NADPH-sulfite redu	sulfite reductase	NADPH-ferrihemopro	nitric-oxide synth												
SUMMARIES	an T	A34286	A69975	D69799	T40056	S29123	538427	T37567	G70040	A83726	JC7192	RDPGO4	A60557	S27158	A25505	S46735	S37156	T14903	A47298	T05582	S37159	T14904	T10771	T39378	S37157	A28577	G82674	B82329	T10720	5090NC
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% Query	Match	100.0	2.7	2.0	1.5	1.5	1.4	1.2	1.2	1.2	1.2	1.1	1.1	1.1	1.1	1.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
ć	Score	1048	28	21	16	16	15	13	13	13	13	12	12	12	12	12	11	11	11	11	11	11	10	10	10	10	10	10	10	10
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nitric-oxide synth	nitric-oxide synth	ferredoxin-NADP re	ferredoxin-NADP re	probable ferredoxi	probable cytochrom	NADPH-ferrihemopro	NADPH-ferrihemopro	NADPH-ferrihemopro	NADPH-ferrihemopro	NADPH-ferrihemopro	nitric-oxide synth				
S16233	G01946	S53305	T02215	T03758	T06715	A56592	863895	863698	A37890	T10723	A43271	S47647	156575	S38253 ·	153165
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10	10	6	0	6	σ	σ	6	6	σ	6	6	6	6	6	6
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1 A34286 NADPH-ferri	RESULT 1 A34286 NADPH-ferrihemobrotein reductase (EC 1.6.2.4) - Bacillus megaterium
	N;Contains:	
	C; Date: 10-;	C;Darce: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002 C:Darcesion: 134786: c4365:
	R; Ruettinge	. A.T.; Wen, L.P.; Fulco, A.J. m. 264, 10987-10965, 1989
	A; Title: Co	A: Title: Odding nucleotide, 7 regulatory, and deduced amino acid sequences of P-450-A:Reference number: 34.286. MITD:80.291834: PMTD:25.4658
	A; Accession: A34286 A; Molecule type: DN	A;Accession: A34286 A;Molecule type: DNA
•	A;Residues: A:Cross-ref	1-1049 <rue> prences: GB:J04832: NTD:g142797: PIDN:AAA87602.1: PID:g142798</rue>
	R; Munro, A.1	R; Munro, A.W.; Lindsay, J.G.; Coggins, J.R.; Kelly, S.M.; Price, N.C. FEBS Lett 343, 70-74, 1946
	A; Title: Structural	ructural and enzymological analysis of the interaction of isolated domains
	A; Relefence number: A; Accession: S43653	number: 543653; MULD:94213/10; PMID:8163021 : S43653
	A; Molecule	A; Molecule type: protein
	C; Genetics:	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
	A; Gene: CYP102	Gene: CYP102 Smearfamily: DASO hifmetional ensume CVD102: entechareme DASO homelony: flavodowin
	C; Keywords:	Keywords: chromoprotein; electron transfer; FAD; flavoprotein; FMN; heme; iron; met
	F; 262-423/D F; 483-1046/1	F;262-423/Domain: cytochrome P450 homology <p45> F;483-1046/Domain: NADPH-ferrihemoprotein reductase homology <feh></feh></p45>
	F;485-622/D	F;485-622/Domain: flavodoxin homology <flx> F;401/Binding site: heme iron (Cys) (axial ligand) #status predicted</flx>
-	Query Match	08;
	Best Loca. Matches 1	Best Local Similarity 100.0%; Pred. No. 0; Matches 104%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Qy	1 TIKEMPQPKTFGELKNLPLLINTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60
	Db	2 TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 61
	Oy	61 ACDESRFDKNLSQALKEVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMAY 120
	qq	62 ACDESREDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAWKGYHAMMV 121
	0y 1:	121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA 180
	da da	122 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA 181
	0y 18	181 LDEAMNKLQRANPDDPAYDENKRQFQEDIKVWNDLVDKIIADRKASGEQSDDLLTHMLNG 240
	Db 18	182 LDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG 241
	Oy 24	241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300

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N.Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC 5.5pecies: Bacillus subtilis
C;Date: 21-3u1-2000 #sequence_revision 21-3u1-2000 #text_change 03-3un-2002
C;Accession: A69975
R;Kunst, F; Ogasawara, N; Moszer, I.; Albertini, A.m; Alloni, G; Azevedo, V.; Berter
C; Beron, S; Brouillet, S; Bruschi, C.V. Caldwell, B; Capuano, V; Carter, N.M.; Chd
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A; Authors: P; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Laszevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
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akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Sexiguoni, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Othiya T.; Winters, P.; Wipat, A.; Tamanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Othiya T.; Winters, P.; Wipat, A.; Tamanaka, T.; Tamanaka, T.; Yasumoto, K.; Yasumoto, K.; Yasu, K.; Yasuha, A.; Muthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A.; Accession: R6980; MUID:98044033; PMID:9384377
A.; Reference number: A6980; MUID:98044033; PMID:9384377
A.; Residues: nucleic acid sequence not shown; translation not shown
A.; Molecule type: DNA
A.; Residues: 1-1054 < KUN>

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Cytochrome P450 / NADPH-cytochrome P450 r homolog yetO - Bacillus subtilis
C;Species: Bacillus Signalis
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Ber C; Bron, S; Broulliet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M;
A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A; Athiors: Foulger, D.; Fritz, C.; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Gal
A; Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Levine, A.; Liu, H; Masuda, S.; Mau
Y, M; Ogawa, K; Ogiwara, A.; Oudega, B; Park, S.H; Parro, V; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Setowska, A.; Sea akeuchi, M.; Tamakoshi, A.; Tamaka, H.; Tamaka, H.; Tamaka, H.; Tamaka, H.; Tamaka, H.; Tamaka, H.; Tamama, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Atters, P.; Winters, P.; Wipat, A.; Yamanecto, H.; Yamane, K.; Yasaunoto, N.; Yata, K.; Yata, K.; Yasau, K.; Asaa, K.; Asteence number: A69580; MUID:98044033; PMID:9384377
A; Accession: D69799
A; School of the Gram-Positive bacterium Bacillus subtilia and A; Ances number: A69580; MUID:98044033; PMID:9384377
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A, Residues: 1-1061 < KUN>
A, Cross references: GB: 299107; GB: AL009126; NID: 92632866; PIDN: CAB12544.1; PID: 926330
A, Cross references: GB: 299107; GB: AL009126; NID: 92632866; PIDN: CAB12544.1; PID: 926330
A, Experimental source: strain 168
C, Genetics:
C, Genetics:
C, Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin
C, Reywords: chromoprotein; flavoprotein; heme; iron; metalloprotein
F; 264 425. Momain: cytochrome P450 homology < P45>
F; 264 425. Momain: cytochrome P450 homology < P54>
F; 493-1057. Momain: glavodoxin homology < P5.
F; 495-632. Momain: flavodoxin homology < P5.
F; 403. Milliang site: heme iron (Cys) (axial ligand) #status predicted
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchl, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
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Matches 28; Conservative
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146 DMTRLTLDTIGLCGFNYRFNS 166

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NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger
N;Alternate names: NADPH-cytochrome P450 oxidoreductase
C;Species: Aspergillus niger
C;Species: Aspergillus niger
C;Accession: S38427
R;van den Brink, J.; van Zeijl, C.; van den Hondel, C.; van Gorcom, R.
submitted to the EMBL Data Library, October 1993
A;Description: Cloning and characterization of the NADPH cytochrome P450 oxidoreducta
A;Accession: S38427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 595/3
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo
C;Keywords: flavoprotein; NADP; oxidoreductase
F;66-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;66-220/Domain: flavodoxin homology <FLX>
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A;Introns: 45/3; 71/3; 111/2
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo
C;Keywords: flavoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable NADPH cytochrome reductase - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #text_change 31-Mar-2000
C; Accession: T37567
R; Wood, V; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
R; Wood, V; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
R; Wood, V; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
R; Wood, V; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
R; Mood, V; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
R; Mood of the EMBL Data Library, February 1999
R; Reference number: Z21725
R; Accession: T37567
R; Reference number: Z21725
R; Accession: T37567
R; Reference number: Z21725
R; Reference number: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-693 <VAN>
A;Cross-references: EMBL:Z26938; NID:g408110; PIDN:CAA81550.1; PID:g408111
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1.2%; Score 13; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 13; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
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S.Suberfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemopro
C; Superfamily: NADPH-ferrihemoprotein reductase homology cFEH>
E; 53-677/Domain: NADPH-ferrihemoprotein reductase homology cFEH>
F; 55-208/Domain: flavodoxin homology <FLX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 2
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprd
C;Keywords: flavoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - fission yeast (Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAILETINGUISTO CONTINUENCE TO CONTINUENCE PORTOR NAILE CONTINUENCE PORTOR NAILETINGUIST CONTINUENCE PORTOR NAILETINGUIST CONTINUENCE PORTOR C'Species: Schizosaccharomyces pombe C'Species: Schizosaccharomyces pombe C'Species: Schizosaccharomyces pombe C'Species: Schizosaccharomyces pombe C'Species: S29123; T40324; S20814

R;Miles, J.S.
Biochem. J. 287, 195-200, 1992

A;Title: Structurally and functionally conserved regions of cytochrome P-450 reductase ascharomyces pombe CDNA.

A;Reference number: S29123; MUD: 93038553; PMID: 1417773

A;Accession: S29123

A;Residues: 1-678 <MIL>
                                  nadph-cytochrome p450 reductase - fission yeast (Schizosaccharomyces pombe) (fragment)
                                                                         C; Species: Schizosaccharomyces pomber (Species: Schizosaccharomyces) (Inagment C; Species: Schizosaccharomyces pomber (State: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 09-Jun-2000 C; Accession: T40056 M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F. A; Reference number: 221903 A; Reference number: 221903 A; Reference number: 221903 A; Reference number: 221903 A; Residues: T-40056 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-661 <LXN> A; Residues: 1-661 <LXN> A; Residues: EMBL: AL034463; PIDN: CAA22429.1; GSPDB:GN0067; SPDB:SPBC29A10.01 A; Experimental source: strain 972h-; cosmid c29A10 C; Genetics:
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A; Residues: 1-678 cwOo>
A; Cross-references: EMBL:AL078627; PIDN:CAB44769.1; GSPDB:GN00067; SPDB:SPBC365.17
A; Experimental source: strain 972h-; cosmid c365
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100.0%; Pred. No. 6.9e-07;
tive 0; Mismatches 0;
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100.0%; Pred. No. 6.7e-07;
Live 0; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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es 16; Conserv
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Hes 16; Conserv
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Best Local S
Matches 16
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Gaps

Best Loc Matches

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Length 710;

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A. Woolecule type: protein
A. Residues: 1-677 < HAN>
A. Reference brancher: 400403; MUID:87075664; PMID:3098240
A. Reference number: A00403; MUID:87075664; PMID:3098240
A. Reference number: A00403; MUID:87075664; PMID:3098240
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162. S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 4
                                                                                            A;Accession: JC7192
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-710 < TABD>
A;Cross-references: (B:AF195659
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo
C;Keywords: flavoprotein; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - pig
N;Alternate names: NADP-cytochrome P450 reductase
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1986 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
C;Accession: A25584; A00403
R;Hanlu, M.: Iyanagi, T.; Miller, P.; Lee, T.D.; Shively, J.E.
Bjochemistry 25, 7906-7911, 1986
A;Title: Complete amino acid sequence of NADPH-cytochrome P-450 reductase from porcin A;Reference number: A25584; MUID:87101085; PMID:3098837
                       A;Title: Cloning and characterization of the cytochrome P450 oxidoreductase gene from A;Reference number: JC7192; MUID:20145435; PMID:10679206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13; DB 2; LA Pred. No. 0.00065;
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Best Local Similarity 100.(
Matches 13; Conservative
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A;Residues: 2-677 <HAN>
A;Note: 551-Gln was also found
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Matches 12; Conservative
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 0.1-Dec-2000 $sequence_revision 01-Dec-2000 $text_change 03-May-2002
C;Accession: A83726
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira R;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hibert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapdus, A.; Laulionins, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogdwa, K.; Ogdwa, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteclel Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron A; Winters, P.; Wipat, A.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Tamanoto, H.; Yasumoto, K.; Yata, K.; Yata, K.; Yoshida, R.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Tarestene number: Asserterium Bacillus subtilis. A; Accession: G70040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH-ferrihemoprotein re
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-607 < SSTO>
A; Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04328.1; GSPDB:GN0C
A; Experimental source: strain C-125
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C;Keywords: flavoprotein
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A;Molecule type: DNA
A;Residues: 1-605 < KURD.
A;Cross-references: GB:Z99121; GB:AL009126; NID:92635827; PIDN:CAB15349.1; PID:92635857
A;Experimental source: strain 168
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NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Cunninghamella elegans
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Cunninghamella elegans
C;Species: Cunninghamella elegans
C;Species: O3-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 03-Jun-2002
C;Accession: JC7192
R;Yadav, J.S.; Loper, J.C.
Blochem. Blophys. Res. Commun. 268, 345-353, 2000
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F;68-604/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;70-209/Domain: flavodoxin homology <FLX>
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100.0%; Pred. No. 0.00056;
tive 0; Mismatches 0; Indels
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R;Yamano, S.; Aoyama, T.; Mcbride, O.W.; Hardwick, J.P.; Gelboin, H.V.; Gonzalez, F.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Homo sapiens (man)
C; Species: 17-Apr. 1993 * * Resquence_revision 31-Dec-1993 * text_change 03-Jun-2002
C; Date: 17-Apr. 186957; S21686
R; Haniu, M.; McManus, M.E.; Birkett, D.J.; Lee, T.D.; Shively, J.E.
Blochemistry 28, 8639-8645, 1989
A; Tile: Structural and functional analysis of NADPH-cytochrome P-450 reductase from A; Reference number: A33421; MUID:90105390; PMID:2513880
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1.1%; Score 12; DB 1;
100.0%; Pred. No. 0.006;
tive 0; Mismatches (
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A,Molecule type: mRNA
A,Residues: 1-679 <RMY>
A,Residues: 1-679 <RMY>
A,Cross-references: GB:X04610; NID:g1543; PIDN:CAA28279.1; PID:g1544
B,Black, S.D.; Coon, M.J.
J. Biol. Chem. 257, 5929-5938, 1982
A,Tifle: Structural features of liver microsomal NADPH-cytochrome P-450 reductase. Hy
A,Reference number: A05233; MUID:82167456; PMID:6802823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Molecule type: protein
A; Residues: 'PTHDG',14-39,'NY',42-52,'N',54-81 <BLA>
A; Residues: 'PTHDG',14-39,'NY',42-52,'N',54-81 <BLA>
A; Note: the order of the first four residues was not determined
A; Note: the amino end of the mature protein is acetylated
C; Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of
C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo
C; Reywords: acetylated amino end; electron transfer; FAD; flavoprotein; FMN; membrane
F; 78-228/Domain: membrane-bound #status predicted <FMN>
F; 78-228/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
                                                                                                                                                                    R;Kātagirī, M.; Murakami, H.; Yabusaki, Y.; Sugiyama, T.; Okamoto, M.; Yamano, T.; Oh
J. Biochem. 100, 945-954, 1986
A;Title: Molecular cloning and sequence analysis of full-length cDNA for rabbit liver
A;Reference number: A25505; MUID:87137361; PMID:3029050
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A; Residues: 1-691 < DNZ>
A; References: EMBL: U000062; NID: 9488162; PIDN: AAB68904.1; PID: 9488169; GSPDB: GNO
B; Ycloss-references: EMBL: U00062; NID: 9488162; PIDN: AAB68904.1; PID: 9488169; GSPDB: GNO
B; A; Dochem: 103, 1004-1010, 1988
A; Title: Primary structure of Saccharomyces cerevisiae NADPH-cytochrome P450 reductas
A; Reference number: A41447; MUID: 89008184; PMID: 3139648
A; Accession: A41447
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N;Alternate names: NADP-cytochrome P450 reductase; protein H8179.8; protein YHR042w
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C;Accession: S46735; A41447; B41447
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A;Resdidues: 1-422,'N',424-473,'G',475-691 <YAB>
A;Cross-references: GB:D13788; GB:D00316; NID:g218452; PIDN:BAA02936.1; PID:g218453
A;Accession: B41447
                                             NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - rabbit
C;Species: Oryctclagus cuniculus (domestic rabbit)
C;Date: 05-Oct-1988 *sequence_revision 05-Oct-1988 *text_change 03-Jun-2002
C;Accession: A25505, A05233
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F:88-96/Regolon: FMN-Phosphate binding #status predicted
F:268-327,453-478/Domain: FAD binding #status predicted <FAD>
F:294-297/Region: FAD-pyrophosphate binding #status predicted
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100.0%; Pred. No. 0.006;
tive 0; Mismatches 0; Indels
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A; Description: The sequence of S. cerevisiae cosmid 8179.
A; Reference number: $46732
A; Accession: $46735
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A;Cross-references: MIPS:YHR042w; SGD:S0001084
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Best Local Similarity 100.
Matches 12; Conservative
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A; Residues: 2-13;45-62 <YA2>
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A; Residues: 2-499, 'V.501-517, 'L',519-536, 'WH',539-677 < SHE>
A; Residues: 2-499, 'V.501-517, 'L',519-536, 'WH',539-677 < SHE>
A; Cross-references: GB:S90469; NID:9247307
A; Cross-references: GB:S90469; NID:9247306; PIDN:AAB21814.1; PID:9247307
C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase #status experimental CAMIN-
F; 1-56/Domain: membrane-bound #status predicted < FMN>
F; 2-677/Product: NADPH-ferrihemoprotein reductase #status experimental < MAIN-
F; 80-675/Domain: FMN binding #status predicted < FMN>
F; 80-675/Domain: FMN binding #status predicted < FMN>
F; 84-254/Domain: FMN phosphate binding #status predicted < FMD-
F; 84-256/Region: FMN-phosphate binding #status predicted < FMD-
F; 84-256/Region: FMN-phosphate binding #status predicted < FMD-
F; 85-3256/Region: FMN-pyrophosphate binding #status predicted < FMD-
F; 85-3256/Region: FMD-pyrophosphate binding #status predicted < FMD-
F; 866/Binding site: Acetylated amino end (Gly) (in mature form) #status experimental F; 566/Binding site: NADP (Cys) #status experimental
          DNA cloning, sequence and vaccin
                                                                                                 A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-137, 'G', '139-577, 'DV', 580-677 < YAM>
A; Residues: 1-137, 'G', '139-577, 'DV', Segall, H.J.; Phillips, I.R.
B; Shephard, E.A.; Palmer, C.N.A.; Segall, H.J.; Phillips, I.R.
Arch. Blochem. Biophys. 294, 168-172, 1992
A; Title: Quantification of cytochrome PA50 reductase gene expression in human tissues.
A; Reference number: S21686; WUID:92198003; PMID:1550342
A; Accession: S21686
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100.0%; Pred. No. 0.006;
ive 0; Mismatches 0; Indels
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Pred. No. 0.006;
0; Mismatches 0; Indels
A;Title: Human NADPH-P450 oxidoreductase: complementary A;Reference number: A60557; MUID:89313720; PMID:2501655 A;Accession: A60557
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Length 679;

C; Function:

A; Description: electron transfer; oxidoreductase C; Superfamily: NADPH-ferrihemopro C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein C; Keywords: electron transfer; endoplasmic reticulum; flavoprotein; NADP; oxidoreductase F; 61-690 /Domain: NADPH-ferrihemoprotein reductase homology <FEH> 0; Gaps Query Match
1.1%; Score 12; DB 1; Length 691;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 0; Indels

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Search completed: May 29, 2003, 08:44:50 Job time : 50 secs

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May 29, 2003, 08:32:22 ; Search time 26 Seconds (without alignments) 1671.815 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                 OM protein - protein search, using sw model
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US-10-031-146-2 1048 1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 112892 seqs, 41476328 residues OLIGO Gapop 60.0 , Gapext 60.0 0 Title: Perfect score: Sequence: Scoring table: Word size : Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

112892

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_40:\* Database :

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Y556_SYNY3 ANKH_CHRVI TMPB_TREPA TMAP_PYRAB C13B_XYLFA CDXE_STRGO CPXE_STRGO
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HRDKTIWGDDVEEFRPERFERPSAIPQHAFKPFGNGQRACIGQOFALHEATLVLGMMLKH 420
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                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        Biochemistry 40:13456-13465(2001).

-!- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. CATALYSES HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1, OMEGA-2 AND OMEGA-3 POSITIONS, WITH OPTIMUM CHAIN LENGTHS OF 14-16 CARBONS (LAURIC, MXRISTIC, AND PALMITIC ACIDS). THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; IPR001308; Cytochrome_P450.
R InterPro; IPR001309; FRD_binding.
R InterPro; IPR001309; FRD_binding.
R InterPro; IPR001309; FRD_cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
R Pfam; PF00175; NAD_binding; 1.
R Pfam; PF00067; FAD_binding; 1.
R Pfam; PF0067; FAD_binding; 1.
R Pfam; PF0067; FAD_binding; 1.
R PRINTS; PF00031; FPRCR.
R PRINTS; PR0031; FPRCR.
W PROSITE; PS00086; CYTOCHROME_P450; 1.
R PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                        oxidized flavoprotein + H(2)0.
COFACTOR: FAD AND FMN.
SIMILARIY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME P450 FAMILY:
                                                                                         CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                      ferrocytochrome.
CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH
"Pivotal role of water in the mechanism of P450BM-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOCHROME P450.
NADPH-P-450 REDUCTASE.
HEME.
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PDB; 2BMH; 31-UTU-94.
PDB; 1FAG; 12-FEB-97.
PDB; 1BMT; 12-FEB-97.
PDB; 1BWT; 23-SEP-98.
PDB; 1BVY; 23-FEB-99.
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Query Match
 HTAFSRMPNOPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020
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FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480
                                                                                                                   AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
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                                                                                                                                                    DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL
               PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR
                                                                                  GEADASODFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG
                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable bifunctional P-450:NADPH-P450 reductase 2 [Includes:
CYCChrome P450 102 (EC 1.14.14.1); NADPH-Cytochrome P450 reductase (EC 1.6.2.4)].
CYPE OR CYPLO2A3.
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Sequence of the Bacillus subtilis genome region in the vicinity the lev operon reveals two new extracytoplasmic function RNA polymerase sigma factors Sigv and Sigz.";
Microbiology 143:2939-2943(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
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R. Boutliss R. Soutsier L., Breas A., Braun W., Brighell S.C., Ren S.,
R. Britan K. D., Errington J., Rabret C., Ferrart E. Foughten M., Johnsel R.A.,
Benitan K. D., Frington J., Rabret C., Ferrart E. Foughten M., Johnsel R.A.,
Benitan K. D., Frington J., Rabret C., Ferrart E. Foughten M., Johnsel M.,
R. Britan K. D., Frington J., Rabret C., Fallerin M., Johnsel M.,
Benitan K. D., Frington J., Rabret C., Fallerin J., Galleron N.,
R. Billerin H., Rolisappel S., Resono S., Malchilly E.J., Catand C. N.,
R. Guissepl G., Ogy B.J., Maga K., Malch M., Fillo M.F., Ligha M., Johnsel M.,
R. Guissepl G., Ogy B.J., Maga K., Johnsel M., Barbot C.R., Heant A.,
R. Guissepl G., Mass M., Mellad M., Johnsel M., Mandon M.,
R. Lee S. M., Levine A., Lill H., Massada S., Massel C., Maskel S., Massel M.,
Roome D., Or Railly W., Demands A., Lardinold S., Lauber J., Lazarweit V.,
R. Ressena E., Polic P., Purnalla B., Rapport G., Ray M., Raynolds S.,
R. Ressena E., Polic P., Purnalla B., Rapport G., Ray M., Raynolds S.,
R. Ressena E., Polic P., Purnalla B., Rapport G., Ray M., Raynolds S.,
R. Restudin N., Tamakoshi A., Tanaka T., Terpsitz B., Toggnoni A.,
R. Harta A., Wambutt R., Yanaka H., Yanaka T., Terpsitz B., Toggnoni A.,
R. Harta A., Wambutt R., Yanaka H., Yanaka H., Yanaka H., Mandoni M.,
R. Harta S., Wandutt R., Yanaka H.F., Zumsten E., Wassing C. R., Yoshkawa H.F., Zumsten E., Wassing C., Yata K.,
R. Manters P., Wipht M., Pamakoshi A., Tanaka T., Terpsitz B., Toggnoni A.,
R. Manters P., Wipht M., Reduce E., Medler E., Wodler E., Yoshkawa H.F., Zumsten E., Wassing C.,
R. Yoshkawa H.F., Zumsten E., Robert B., Wassing C.,
R. Wassing M., Yoshkawa H.F., Zumsten E., Toggnoni A.,
R. Wassing M., Yanaka H.F., Zumsten E., Yoshkawa H.F., Zumsten E.,
R. Wassing M., Yanaka S., Kanaka M., Walka B., Wassing C.,
R. Wassing M., Yanaka S., Kanaka M., Walka B., Wassing C.,
R. Wassing M., Yanaka S., Raynaka M., Walka B., Wassing C.,
R. Wassing M., Wassing M., Wassing M., Wassing C
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouilaet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouilaet S., Bruschi C.V., Candwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C.C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C.C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Kobyasahi Y., Kootter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kobyasahi Y., Kootter P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Ruita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Saklguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tarkapisth H., Takemasth H., Takemath R.,
Rostovin M., Tacconi E., Takagi T., Takaghashi H., Takemath R.,
Rostovin M., Tacconi E., Takagi T., Takaghashi H., Takemath R.,
Rostovin M., Tacconi E., Takagi T., Takaghashi H., Waitzenegger T.,
RA Wanbutt R., Wedler H., Weitzenegger T.,
RA Wanbutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamano K., Yasumoto K., Yata K.,
Prescent P., Wipat A., Yamamoto H., Yamano K., Yasumoto K., Yata K.,
Preschi W., Presc
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                                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable bifunctional P-450:NADPH-P450 reductase 1 [Includes:
Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97453479; PubMed-9308178; Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J., Borotin A., Purnelle B., Hilbert H., Lauber J., Duesterhoeft A., Ehrlich S.D.; "Sequence of the Bacillus subtilis genome region in the vicinity of the Lev operon reveals two new extracytoplasmic function RNA Microbiology 143:2939-2943(1997).
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-!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID-1423;
                               ö
  100.0%; Pred. No. 9.3e-20;
                                                                                                                                                                                                                                                                         1061 AA.
                            0; Mismatches
                                                                                                           252 LDDENIRYQIITFLIAGHETTSGLLSFA 279
                                                                               249 LDDENIRYQIITFLIAGHETTSGLLSFA 276
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98044033; PubMed-9384377;
                   28; Conservative
                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997)
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYPD OR CYP102A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-168;
                                                                                                                                                                                                                                                                         CYPD_BACSU
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                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
-1- COFACTOR: FAD AND FWN (By similarity).
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Structurally and functionally conserved regions of cytochrome P-450 reductase as targets for DNA amplification by the polymerase chain reaction. Cloning and nucleotide sequence of the Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-2002 (Rel. 21, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADPH-Cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
CCR1 OR SPBC29All0.01 OR SPBC365.17.
SChizosaccharcmyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        475 1061 NADPH-P-450 REDUCTASE.
403 403 HEME (BY SIMILARITY).
1061 AA; 119467 MW; 7915DACC20578978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Leus
. 1.3e-12;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                  Subtilist, BG12871; cypD.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003097; FAL_binding.
InterPro; IPR001079; FAL_cyt_redctse.
InterPro; IPR001226; Flavodoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00258; flavodoxin; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00371; FPNCR.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 DMTRLTLDTIGLCGFNYRFNS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 DMTRLTLDTIGLCGFNYRFNS 164
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MEDLINE-21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00175; NAD_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lochem. J. 287:195-200(1992)
                                                                                                                                                                                                                                                                                                                       EMBL; D87979; BAA20123.1; -. EMBL; Z99107; CAB12544.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.0%;
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SEQUENCE FROM N.A.
                                                       P450 FAMILY.
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Best Local
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RA Sgouros J., Peat N., Rajandream M.A., Lyne M., Lyne R., Stewart A., RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Stollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Anones R., Jones M., Leather S., McDonald S., McLean J., RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA Batter K., O'Neil S., Ranagodi K., Rutherford K., Rutter S., Squares S., Stevens K., Statp S., Stevens K., Raylor R., Volckert G., Aert R., Robben J., Grymonprez B., RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rahler K., Purnelle B., Goffeau A., Canger H., Membutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J., Moreno S., Armstrong J., Forsburg S.L., Ra Daga R.R., Cruzado L., Jimene J., Sanchez M., Garzon A., Thode G., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., Ra Rattell B.G., Nurse P., Ra The genome sequence of Schizosaccharomyces pombe.";

R. The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0369; FLAVODOXIN.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPERES HONOLOGUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FWN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6AEDDFBA6DE39C8F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P)
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Pfam; PF00258; flavodoxin; 1.
Pfam; PF00667; FAD_binding; 1.
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317
448
553
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HSSP; P00388; 1AMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ferrocytochrome.
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306
306
437
535
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678 AA;
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SEQUENCE
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NP_BIND
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Gaps

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1.5%; Score 16; DB 1; Length 678; 100.0%; Pred. No. 1.1e-07; ive 0; Mismatches 0; Indels

Conservative

Local Similarity nes 16; Conserv

Best Loca Matches

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murakami H.O., Ogawa H., Nisimoto Y.; "cDNA closhing and characterization of NADPH-cytochrome P-450 reductase in human HL-60 cell."; Eubmitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92198003; PubMed=1550342;
Shephard E.A., Palmer C.N., Segall H.J., Phillips I.R.;
"Quantification of cytochrome P450 reductase gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                           Haniu M., McManus M.E., Birkett D.J., Lee T.D., Shively J.E.; "Structural and functional analysis of NADPH-cytochrome P-450 reductase from human liver: complete sequence of human enzyme and NADPH-binding sites."
                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                         P16435; Q16455; Q9H3M8;
01-AUG-1990 (Rel. 15, Created)
10-AUG-1990 (Rel. 15, Last sequence update)
15-UNW-2002 (Rel. 41, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Czerwinski M., Sahni M., Madan A., Parkinson A.; "Polymorphism of human CYPOR: expression of new allele."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arch. Biochem. Biophys. 294:168-172(1992).
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                               MEDLINE-90105390; PubMed=2513880;
                                                                                                                                                                                                                                                                                                                                                                                                              NADPH-binding sites.";
Biochemistry 28:8639-8645(1989).
                  899 IMVGPGTGVAPFRGFV 914
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                                                                                                               STANDARD;
                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ferrocytochrome
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Ohgiya S., Ishizaki K., Kamataki T., Shinriki N.;
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NP_BIND
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                       Endoplasmic reticulum;
                                                                                                                                                                                                                                   ACETYLATION.
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Obdiya S., Goda T., Ishizaki K., Kamataki T., Shinriki N.; "Molecular cloning and sequence analysis of guinea-pig NADPH-cytochrome P-450 oxidoreductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                       Score 12; DB 1; Length 676; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Obgiya S., Goda T., Ishizaki K., Kamataki T., Shinriki N.;
Biochim. Biophys. Acta 1174:313-313(1993).
                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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M -> L (IN REF. 4).

F -> L (IN REF. 2 AND 4).

T -> T (IN REF. 2 AND 4).
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883EA13797020D70 CRC64;
                                                                                                                                                                                 PRINTS; PR00369; FLAVODOXÍN.
PRINTS; PR00311; FPNCR.
Oxidoreductaes; Flavoprotein; FMN; FAD; NADP; Endc
Membrane; Acetylation; Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                       /FTId=VAR_004617.
R -> Q.
/FTId=VAR_004618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      677 AA.
                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ...
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                                                                                                 InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001094; Flavddxin_like.
InterPro; IPR001226; Flavddxin,
InterPro; IPR00133; Oxred_FAD_NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavddoxin; 1.
Pfam; PF00567; PAD_binding; 1.
                                                                                                                                                                                                                                                                                               A -> V.
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MEDLINE-93041995; PubMed-1420354;
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                                       EMBL; AF258341; AAG09798.1; -. EMBL; AA051763; BAB18572.1; -. PIR; A33421; A33421. PDB; IBIC; 24-NOV-99.
                                                                                                                                                                                                                                                                                                                                                                     76558 MW;
                             EMBL; S90469; AAB21814.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                899 IMVGPGTGVAPF 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 IMVGPGTGVAPF 539
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.1
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                  550
                                                                                HGNC:9208; POR.
                                                                                                                                                                                                                                                                                                                                                                   676 AA;
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517
536
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-i- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
Membrane; Acetylation.
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                                                                                                                                                                                                                                                                                                                                                         -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO ORIGINATE FROM MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
ACCTULATION (BY SIMILARITY).
FWN (PYRINDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                 -i- SUBCELLUIAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-i- SIMILEMITRY: THE FAM-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                        TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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01-JUN-1994 (Rel. 29, Last sequence update)
16-0CT-2001 (Rel. 40, Last amotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
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Conservative 0; Mismatches
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HSSP; P0388; LAMO.
InterPro; IPR003097; FAD_binding,
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR0011094; Flavdoxin_like.
InterPro; IPR00125; Flavdoxin_like.
InterPro; IPR001433; Oxred_FAD/NAD(P).
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MEDLINE-94281246; Pubmed-8011664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00175; NAD binding; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00667; FAD_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76650 MW;
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                                                                                                                                               -1- COFACTOR: FAD AND FMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                899 IMVGPGTGVAPF 910
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460
547
640
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                                                                                                                    ferrocytochrome.
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529
624
677 AA;
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Matches 12; Conserv
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P37040;
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MOD_RES
NP_BIND
NP_BIND
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
         functional expression in yeast.";
Blochim. Blophys. Acta 1186:137-141(1994).
-!- FUNCTION: THIS ENIXME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
-!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00359; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FNN; FAD; NADP; Endoplasmic reticulum;
"Mouse NADPH-cytochrome P-450 oxidoreductase: molecular cloning and
                                                                                                 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER MEMBRANE BY ITS N.TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FAN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOWOLOGUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLATION (BY SIMILARITY).
FEMN (PYRIMIDIDE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
0065C14D0E1C5EF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12; DB 1; Length 677;
Pred. No. 0.0013;
0; Mismatches 0; Indels
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Cetartiodactyla, Suina, Suidae,
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Last annotation update
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Interpro; IPR001709; FPN_cyt_redetse.
Interpro; IPR001094; Flavdaxin_like.
Interpro; IPR001226; Flavdaxin_like.
Interpro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; Nab_binding; 1.
Pfam; PF00258; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Scc.
100.0%; Pre
0; '
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                                                                                                                                                                                                                                                                                                   SWISS-2DPAGE; P37040; MOUSE.
MGD; MGI:97744; Por.
                                                                                         -1- COFACTOR: FAD AND FMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  899 IMVGPGTGVAPF 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Membrane; Acetylation INIT_MET 0
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169
313
450
529
624
677 AA;
                                                                                ferrocytochrome
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                                                                                                                                                                                                                                                                                         P00388; 1AMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                           REDUCTASE
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P04175;
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NP_BIND
SEQUENCE
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NP_BIND
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. J. 236:871-878(1986).
-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO STOCHOME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
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PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                        MEDLINE-87075664; PubMed-3098240;
Vogel F., Lumper L.;
"Complete structure of the hydrophilic domain in the porcine NADPH-
cytochrome P-450 reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-1- SIMILARITY: THE FWN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                         MEDLINE-87101085; PubMed-3099837;
Hanlu M., Iyanagi T., Miller P., Lee T.D., Shively J.E.;
Complete amino acid sequence of NADPH-cytochrome P-450 reductase
from porcine hepatic microsomes.";
Blochemistry 25:7906-7911(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2 ferrocytochrome.
Amborn J., Preiss B., Stender B., Viale M., Repp R.Z., Lampert Stroger M., Lumper L.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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T -> A (IN REF. 3).

D -> D (IN REF. 3).

N -> D (IN REF. 3).

R -> L (IN REF. 3).

N -> D (IN REF. 2).

V -> L (IN REF. 2).

V -> L (IN REF. 2).

Z -> N (IN REF. 3).

Z -> N (IN REF. 3).

Z -> N (IN REF. 3).
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InterPro; IPR003097; FAD_binding,
InterPro; IPR00109; FNC_cyt_redectse.
InterPro; IPR001094; Flavdoxin_lke.
InterPro; IPR001265; Flavdoxin_lke.
InterPro; IPR001431; Oxred_FAD_NAD(P).
Pfam; PP00175; NAD_binding; 1.
Pfam; PP00258; flavodoxin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A00403; RDPGO4.
PIR; A25584; A25584.
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677 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. Biol. Chem. 257:5929-5938(1982).

-I- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME PASO IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.

-I- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.
                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Black S.D., Coon M.J.; "Structural features of liver microsomal NADPH-cytochrome P-450 reductase. Hydrophobic domain, hydrophilic domain, and connecting
                                                                                                                                                                                                                                                                                                                                                                                                                                  Katagiri M., Murakami H., Yabusaki Y., Sugiyama T., Okamoto M., Yamano T., Ohkawa H.; "Molecular Cloning and sequence analysis of full-length cDNA for rabbit liver NADPH-cytochrome P-450 reductase mRNA.";
                                      ö
                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
1.1%; Score 12; DB 1; Length 677;
100.0%; Pred. No. 0.0013;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                     679 AA.
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InterPro; IPR001709; FPM_cyt_redetse.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NaD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
MEDLINE-87137361; PubMed-3029050;
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MEDLINE-82167456; PubMed-6802823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. 100:945-954(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D00101; BAA00063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: FAD AND FMN.
                                                                 899 IMVGPGTGVAPF 910
                                                                                    EMBL; X04610; CAA28279.1;
PIR; A25505; A25505.
PIR; A05233; A05233.
                                  12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE OF 1-81.
                                                                                                                                                                                     STANDARD;
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                 Similarity
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                                                                                                                                                                                  NCPR_RABIT
P00389;
21-JUL-1986 (
21-JUL-1986 (
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Query Match
                   Best Local
Matches 1
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NCPR_RABIT
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SECUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE-94378003; PubMed-8091229;
MEDLINE-94378003; PubMed-8091229;
MEDLINE-94378003; PubMed-8091229;
Du Z., Favello A., Fulton L., Gattung S., Gelsel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 1-12 AND 44-61.
MEDLINE-89008184; PubMed-3139648;
Yabusaki Y., Murakami H., Ohkawa H.;
"Primary structure of Saccharomyces cerevisiae NADPH-cytochrome P450 reductase deduced from nucleotide sequence of its cloned gene.";
J. Biochem. 103:1004-1010(1988).
                                                                                                                                                                                                                                                                                                                                   Gaps
                                              Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
Membrane; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                           (PYRIMIDINE PART) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 265:2077-2082(1994).
-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM N.
TO CYTOCHROWE P450 IN MACROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
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-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.
                                                                                                                                        FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
YW -> NY (IN REF. 2).
E -> N (IN REF: 2).
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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                                                                                                        FMN (PYRIMIDINE PART) (BY SIMI:
FAD (ADP PART) (BY SIMILARITY)
FAD (FLAVIN PART) (BY SIMILARI'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-FBB-1995 (Rel. 31, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
NCPI OR NCPRI OR PRD1 OR YHR042W.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                       DB 1; Length 679;
0.0013;
hes 0; Indels
                                                                                                                                                                                                                                                 B1A163FA53A5988B CRC64;
                                                                                                                                                                                                                                                                            1.1%; Scot.
100.0%; Pred. No. con.
0; Mismatches
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76588 MW;
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ferrocytochrome.
-1- COFACTOR: FAD AND FMN.
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                                                                                                                                                                                                                                                                                                                                                                                             530 IMVGPGTGVAPF 541
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Best Local Similarity 100.
Matches 12; Conservative
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53
679 AA;
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NP_BIND
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NP_BIND
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NCPR_YEAST
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01-0cr-1994 (Rel. 30, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
16-0cr-2001 (Rel. 40, Last annotation update)
18-0cr-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
Phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                 PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                         FWN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP-PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                         Score 12; DB 1; Length 690;
Pred. No. 0.0013;
0; Mismatches 0; Indels
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-> N (IN REF. 1).
FEFA18F6AB2BBDF5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 0.0 cive 0; Mismatches
                                                                                                     HSSP, 900388, 1AMO.
SGD; SG001084; NCP1.
InterPro; 1PR003097; FAD_binding.
InterPro; 1PR001097; FPN_cyt_redctse.
InterPro; 1PR001094; FPN_cyt_redctse.
InterPro; 1PR001226; Flavodoxin_like.
InterPro; 1PR001226; Flavodoxin.
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00657; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00369; FLAVODOXIN.
                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                     76640 MW;
                                                              EMBL; D13788; BAA02936.1; -. EMBL; U00062; AAB68904.1; -.
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539 GPGTGVAPFRGF 550
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Matches 12; Conservative
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311
445
554
654
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                                                                                      PIR; A41447; A41447.
PIR; S46735; S46735.
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422 4
690 AA;
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P37116;
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NP_BIND
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NCPR_PHAAU
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FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTEWTIAL).
N-LINKED (GLCNAC. . . ) (POTEWTIAL).
W-LINKED (GLCNAC. . . ) (POTEWTIAL).
W-, 592966167E8561DE CRC64;
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                                                                                                                                                                                                                                                                                                               InterPro; IPR001909; FAD_binding.
InterPro; IPR001709; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR00125; Flavodoxin_like.
InterPro; IPR00125; Navedoxin.
InterPro; IPR00133; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00568; FAD_binding; 1.
Primrs; PR00369; FAD_binding; 1.
PRINTS; PR00371; FPNCN.
Oxidoreductase; Flavoprotein; FNN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourcs J., Peat N., Hayles J., Baker S., Basham D., Bowan S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Horneby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quali M.A., Rabhinowitsch E., Skelton J., Simmonds M., Squares S., Stevens K.,
FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, AND GLUTATHIONE REDUCTASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 11; DB 1; Length 690; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein C12C2.03c in chromosome II. SPBC12C2.03c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
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MEDLINE-21848401; PubMed-11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76506 MW;
                                                                                                                                                                                                                                                                          EMBL; L07843; AAA34240.1; -. HSSP; P00388; 1AMO.
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01-NOV-1995 (Rel. 32,
15-JUN-2002 (Rel. 41,
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639
275
339
690 AA;
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ONIA_9N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 009744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
YB63_SCHPO
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Membrane.
NON_TER
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NON_CONS
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOS1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
SETT TENENCY SOLVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
             Woodward J., Volokaert G., Aer R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Puchs M., Fritze C., Holzer E., Moestl D., Hilbert H., A. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Mottier S., Goffeau A., Cadieur E., Dreano S., Gloux S., Lelaure V., Mottier S., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Spackovski G.V., Ussery D., Barrell B.G., Nurse P., Shakkin J., A., Moreno S., Armstrong J., Forsburg S.L., The genome sequence of Schizosaccharomyces pombe.";

"The genome sequence of Schizosaccharomyces pombe.";

"In Stallarity: SOME, TO NADPH-CYTOCHROME P450 REDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Chromatogr. A 397:123-136(1987)

-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
Walsh S.V., Warren T., Whitehead S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: FAD AND FMN.
SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Urenjak J., Linder D., Lumper L.; "Structural comparison between the trout and mammalian hydrophilic domain of NADPH-cytochrome P-450 reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmo trutta (Brown trout).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 10; DB 1; Length 571;
100.0%; Pred. No. 0.12;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Oxidoreductase; Flavoprotein; FAD. SEQUENCE 571 AA; 63976 MW; D2EE992789307249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Created)
1-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_TaxID=8032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 254140; CAA90816.1; -.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
Taylor K., Taylor R.G., Tivey A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88008061; PubMed-3116019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00175; NAD_binding; 1. Pfam; PF00667; FAD_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                906 GVAPFRGFVQ 915
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P19618;
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SO WEND DRAW OF COLOR OF COLOR
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Dev. Neurosci. 19:224-231(1997).

-i- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A NEUROTRANSMITTER. ISOFORM NNOS MU MAY BE AN EFFECTOR ENZYME FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DITLIC OXIGE + N NADP(+).

COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBOOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE BRZYME (BY SIMILARITY).

THE BRZYME (BY SIMILARITY).

REGULATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOS1_MOUSE STANDARD; PRT; 1429 AA.
O9Z0J4; 064208;
09Z0O( Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal NOS) (N-NOS) (CONSTILLTIVE NOS) (NOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Skeletal muscle;
MEDIINE-96212184; PubMed-8626668;
Silvagno F., Xia H., Bredt D.S.;
"Neuronal nitric-oxide synthase-mu, an alternatively spliced isoform expressed in differentiated skeletal muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ogura T., Yokoyama T., Fujisawa H., Kurashima Y., Esumi H.; "Structural diversity of neuronal oxide synthase mRNA in the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE DYSTROPHIN COMPLEX.
CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
                                                                                                                                                                                                                                                            Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97351924; PubMed-9208206;
Brenman J.E., Xia H., Chao D.S., Black S.M., Bredt D.S.;
"Regulation of neuronal nitric oxide synthase through alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE SPLICING (ISOFORMS NNOS BETA; NNOS GAMMA AND NNOS MU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 68304 MW; BC801767DE1D44C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 193:1014-1022(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS N-NOS-1 AND N-NOS-2). STRAIN-BALB/C; TISSUE-Brain; MEDLINE-93312283; PubMed=7686743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 10; DB
100.0%; Pred. No. 0.1
ive 0; Mismatches
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                                                  PIR; A28577; A28577.
HSSP; P16435; 1B1C.
INTERPO; IPR01709; FPN_cyt_redctse.
INTERPO; IPR001709; FPN_cyt_redctse.
INTERPO; IPR001094; Flavdoxin_like.
PRINTS; PR00369; FLAVDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM NNOS MU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                          427
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                                                                                                                                                                                                                                                                                                                                   1
426
434
401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10090;
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SEQUENCE
    VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                -I-TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE NERVOUS SYSTEM:
EXPRESSED IN CEREBRUM, OLFACTORY BULB, HIPPOCAMPUS, MIDBRAIN,
CEREBELLUM, PONS, MEDULLA OBLONGATA, AND SPINAL CORD. ALSO FOUND
IN SKELETAL MUSCLE, WHERE IT IS LOCALIEDD BENEATH THE SARCOLEMA
OF FAST TWITCH MUSCLE FIBERS, AND IN SPLEEN, HEART, KIDNEY, AND
LIVER, N-NOS-1 AND N-NOS-2 ARE FOUND IN ALL PARTS OF THE NERVOUS
SYSTEM. NNOS BETA AND GAMMA OCCUR IN A REGION-SPECIFIC MANNER IN
THE BRAIN AND NNOS BETA EXPRESSION IS DEVELOPMENTALLY REGULATED.
NNOS MU IS ONLY FOUND IN MATURE SKELETAL AND CARDIAC MUSCLES.
-I-INDUCTION: BY CHOLINERGIC AGONISTS ACTING AT INOSITOL PHOSPHATE-
LINKED MUSCARINIC RECEPPORS IN CARRIAC MYCOYTES.
-I-DOMAIN: THE PDZ DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL
ISOFORM PARTICIPATES IN PROTEIN-PROFIEN INTERACTION, AND IS
RESPONSTBLE FOR TARGETING NNOS TO SYNAPTIC MEMBRANES IN WUSCLES.
-I-DISEASE: IN MDX MICE (MOUSE MODEL OF DISTROPHINOPATHY) THE
DYSTROPHIN COMPLEX IS DISRUPTED AND NNOS IS DISPLACED FROM
SARCOLEMAR AND ACCUMULATES IN THE CYTOSOL.
-I-SIMILARITY: BELONGS TO THE NOS FAMILY.
-I-SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEME (BY SIMILARITY).
CALMODULIN-BINDING (POTENTIAL).
FAD (PYRINIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
MADF (ADP PART) (BY SIMILARITY).
MISSING (IN ISOFORM NNOS BETA).
TGIGNO -> MRISSING (IN ISOFORM NNOS BETA).
MISSING (IN ISOFORM NNOS GAMMA).
MISSING (IN ISOFORM NNOS CAMMA).
                      SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: IN SKELETAL MUSCLE, NNOS IS LOCALIZED
BENEATH THE SARCOLEMAN OF FAST-TWITCH MUSCLE FIBER BY ASSOCIATING
WITH THE DYSTROPHIN GLYCOPROTEIN COMPLEX.
ALTERNALIYE PRODUCTS: 5 ISOFORMS; N.NOS-1 (SHOWN HERE), N.NOS-2,
NNOS BETA, NNOS GAMMA AND NNOS MU/MUSCLE-SPECIFIC; ARE PRODUCED BY
ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; NADP; FAD; FWN; Calmodulin-binding; Heme; Alternative splicing; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004030; NO_synthase.
InterPro; IPR001433; Oxred_FAD/NAD(P).
InterPro; IPR001478; PDZ.
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
THE PROTEIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001226; Flavodoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00667; FAD_binding; 1. Pfam; PF02898; NO_synthase; 1. PRINES; PR00369; FLAVODOXIN. PRINES; PR00371; FP0CR. SWART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D14552; BAA03415.1; -. EMBL; S81982; AAB36469.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS60001; NOS; 1
PROSITE; PS50106; PDZ; 1
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NP_BIND
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NP_BIND
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oxidoreductase.";
J. Biol. Chem. 276:37506-37513(2001).
J. Biol. Chem. 276:37506-37513(2001).
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A NEUROTRANSMITTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS) OF 14-125.
MEDLINE-99238BLS; PUMAGA-[1022]915;
Hillier B.J., Christopherson K.S., Prehoda K.E., Bredt D.S., Lim W.A.;
"Unexpected modes of PDZ domain scaffolding revealed by structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM PNNOS).
STRAIN-Fischer 344; TISSUE-Penis;
MEDLINE-96400219; PubMed-8806605;
MAGE T., Fuentes A.M., Garban H., Rajavashisth T., Marquez D.,
Rodriguez J.A., Rajfer J., Gonzalez-Cadavid N.F.;
"Cloning of a novel neuronal nitric oxide synthase expressed in penis
839 839 K -> KYPEPLRFFPRKGPSLSHVDSEAHSLVAARDSQHR
(IN ISOFORM NNOS MU).
1429 AA; 160472 MW; 3782848D65B41BFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOS1_RAT STANDARD; PRT; 1429 AA. P29476; P70594; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal NOS) (N-NOS) (NNOS) (Constitutive NOS) (RC-NOS) (BNOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) - citrulline +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloned and expressed nitric oxide synthase structurally resembles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structure of the FAD/NADPH-binding domain of rat neuronal nitric-oxide synthase. Comparisons with nadph-cytochrome p450
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bredt D.S., Hwang P.M., Glatt C.L., Lowenstein C., Reed R.R.,
Snyder S.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21134290; PubMed-11237702;
Sato Y., Sagami I., Matsui T., Shimizu T.;
"Unusual rolle of Tyr58 of neuronal nitric oxide synthase in
controlling substrate specificity and electron transfer.";
Biochem. Biophys. Res. Commun. 281:621-626(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang J., Martasek P., Paschke R., Shea T., Masters B.S.S., Kim J.-J.P.,
                                                                                                                                   Length 1429;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 963-1397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 226:145-151(1996)
                                                                                                                                          Score 10; DB 1;
Pred. No. 0.27;
                                                                                                                        Ouery Match
Best Local Similarity 100.0%; Fred. No. 0.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21463055; PubMed=11473123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91287795; PubMed=1712077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome P-450 reductase.";
Nature 351:714-718(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and lower urinary tract.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nNOS-syntrophin complex.";
Science 284:812-815(1999).
                                                                                                                                                                                                                                                                                                                  1172 PRYYSISSSP 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                 826 PRYYSISSSP 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS OF TYR-588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum-Brain;
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                                             THE ENZYME (BY STMILLARITY)

-1- ENZYME REGILATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY
N-NOS-INHIBITING PROPERN (FIN) WHICH MAY PREVENT THE DIMERIZATION
OF THE PROTEIN (BY SIMILARITY).
-1- SUBGUNIT: HOMODIMER (BY SIMILARITY).
-1- SUBGLIULAR LOCATION: IN SKELETAL MUSCLE, NNOS IS LOCALIZED
BENEATH THE DYSTROPHIN GLYCOPROTEIN COMPLEX (BY SIMILARITY).
-1- ALTERNATIVE PRODUCES: 3 ISOFORMS, N-NOS-1 (SHOWN HERE), N-NOS-2
AND PRINOS: ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: ISOFORM N-NOS1 IS EXPRESSED IN BRAIN. ISOFORM
HONOS IS EXPRESSED IN THE PENIS, URETHRA, PROSTATE, AND SKELETAL
MUSCLE, AND CORXISTS WITH THE CREBELLAR NNOS IN THE PELVIC
PLEXUS, BLADDER AND LIVER, AND IS DETECTABLE IN THE CEREBELLUM.
-1- DOMAIN: THE PDZ DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL
ISOFORM PARTICIPATES IN PROTEIN-PROTEIN INFERACTION, AND IS
RESPONSIBLE FOR TARGETING NNOS TO SYNAPTIC MEMBRANES IN MUSCLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).

HEME (BY SIMILARITY).

CARBOXYLATE OF THE SUBSTRATE.

CALMODULIN-BINDING (POTENTIAL).

FMN (PYRIMIDINE PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

MISSING (IN ISOPORM N-NOS-2).

K -> KYPPELRFFPRGPSLSHVDSEAHSLVAARDSQHR

(IN ISOFORM PNNOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY
                 COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50% DECREASE OF ACTIVITY 30% DECREASE OF ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS60001; NOS; 1.
PROSITE; PS50106; PD2; 1.
Oxldoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternative splicing; Multigene family; 3D-structure. DOMAIN 17 99 PD2.
                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE NOS FAMILY.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IRR003097; FAD_binding.
InterPro; IRR003097; FAD_binding.
InterPro; IRR001094; Flavdoxin_like.
InterPro; IRR001226; Flavdoxin.
InterPro; IRR004030; NO_synthase.
InterPro; IRR004030; NO_synthase.
InterPro; IRR004133; Oxred_RAD/NAD(P).
InterPro; IRR001478; PDZ.
InterPro; IRR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y->H:
Y->S:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00667; FAD_binding; 1.
Pfam; PF02898; NO_synthase; 1.
PRINTS; PR00369; FLAVODOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X59949; CAA42574.1; -. EMBL; U67309; AAC52782.1; -.
nitric oxide + N NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1QAU; 06-MAR-00.
PDB; 1QAV; 06-MAR-00.
PDB; 1F20; 10-OCT-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S16233; S16233
PDB; 1QAU; 06-MAR-00
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Pfam; PF00667;
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588
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BINDING
DOMAIN
NP_BIND
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VARSPLIC
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MUTAGEN
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Gaps
                                                                                    ö
                                                                Length 1429;
 IN ACTIVITY
                                                                                   Indels
                                             7255C5AE165200F5 CRC64;
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 DECREASE
                                                                 DB 1;
0.27;
       269 I -> V (IN REF. 2
953 P -> A (IN REF. 2
008 F -> S (IN REF. 2
311 A -> V (IN REF. 2
160559 MW; 7255C5AE16520
                                                                Score 10; DB 1; Pred. No. 0.27 0; Mismatches
 Y->F: NO
                                                                         100.08;
                                                                 1.0%;
                                                              Query Match 1.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                1172 PRYXSISSSP 1181
                                                                                                     826 PRYYSISSSP 835
588
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                                             1429 AA;
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Search completed: May 29, 2003, 08:42:08 Job time : 27 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein May 29, 2003, 08:31:47 ; Search time 74 Seconds Run on:

(without alignments)
1887.117 Million cell updates/sec

US-10-031-146-2

Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

908470 seqs, 133250620 residues Searched:

0 Word size :

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*/SIDS2/gcgdata/genseqfyeneseqp-embl/AA1981.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1984.DAT:\*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1985.DAT:\*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1986.DAT:\*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1980.DAT:\*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1987.DAT:\*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1988.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT: /SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT: /SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT; 'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1991.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1992.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998 A\_Geneseq\_101002:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Amino acid sequenc	B. megaterium cyto	B. megaterium cyto	Amino acid sequenc	Bacillus megateriu	P450 17-alpha/P450				
SUMMARIES		•	О	AAB31978	AAB46855	AAB46856	AAY93566	AAB31882	AAB31979	AAB31980	AAB31981	AAY72208	AAR11604
			DB	22	22	22	21	22	22	22	22	22	13
			Match Length DB	1048	1048	1048	1049	1049	1048	1048	1048	1049	1085
	dФ	Query	Match	100.0	100.0	100.0	100.0	100.0	91.7	82.1	82.1	80.7	25.4
			Score	1048	1048	1048	1048	1048	196	860	860	846	266
		Result	No.		7	m	4	S	Q	7	80	6	10

B. megaterium P-45 Cytochrome-P450-ox Human reductase am B. bassiana POPS r Human derived cyto Human derived cyto Mouse ischaemic co Sequence of rabbit Human full-length Rabbit NADH cytoch Human contig polyp Sequence of yeast Mitochondrial cyto Drosophila melanog Helianthus tuberos S. epidermidis ope Staphylococcus epi Poppy cytochrome P Poppy cytochrome P Poppy cytochrome P Poppy cytochrome P Sequence of all or Rat neuronal nitri Rat neuronal nitri Neuronal nitri Neuronal nitri Neuronal nitri Neuronal nitri Neuronal nitri Neuronal nitric cytide	Rat penile neurona Human neuronal nit Drosophila melanog Drosophila melanog Candida tropicalis Candida tropicalis Drosophila melanog Candida tropicalis Candida tropicalis Candida tropicalis Candida tropicalis
4.	3 AAA35566 AAY28476 ABB58868 AAU76367 A AAY90596 ABB64462 ABB64462 ABB64462 ABB7083
78933 1000 1000 1000 1000 1000 1000 1000 1	1463 18 1554 20 516 23 516 23 516 23 679 21 679 22 679 23
64664444444449999999999999999999999999	000000000
	000000000 11
	338 338 442 443 5444 5444

## ALIGNMENTS

AAB31978 ID AAB31978 standard; Protein; 1048 AA. 15-MAY-2001 (first entry) AAB31978; RESULT 1 

Amino acid sequence of a Bacillus P450 monooxygenase protein.

Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin. Bacillus megaterium.

WO200107630-A1.

01-FEB-2001

27-JUL-2000; 2000WO-EP07253.

27-JUL-1999; 99DE-1035115. 18-NOV-1999; 99DE-1055605. 22-MAR-2000; 2000DE-1014085.

(BADI ) BASF AG.

Schmitt J, Fischer M, Schwaneberg U, Hauer B, Pleiss J, Li Q;

Schmid R;

WPI; 2001-182800/18. N-PSDB; AAF54832.

Cytochrome P450 monooxygenase for oxidizing organic compounds, useful

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                                                                                                                                                                                                                                                                                                                                               DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMYRA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         009
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                                           The present sequence represents a cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono or poly-cyclic aromatic heterocyclics containing nitrogen, sulpiur or oxygen; optionally substituted mono or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkenes. The modified cyclohrome P450 monooxygenase are specifically used to oxidize indole to indigo and indorubicin. However, they may be used to oxidise many other substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DIAVQLVQKWERLNADEHIEVPEDWTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA
                                                                                                                                                                                                                                                                                                                                                                                                      1 TIKEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE
                                                                                                                                                                                                                                                                                                 ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDFEDHTNYELDIKETLILKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
                                                                                                                                                                                                                                                                                                                                                                                              LDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL
especially for converting indole to indigo, has wide substrate range
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                     Length 1048;
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                        54pp; German.
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Matches 1048; Conservative
                       Claim 3; Page 35-39;
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This invention describes a novel electron donor system (M1) that transfers electrons to an enzyme with redox properties comprising an inventionation to telectrode-bound, electron sink and a mediator which enable the electron transfer. The invention also describes (1) transferring (M2) oxygen to a hydrocarbon containing hydrogen donor molecule is in a reaction mediator where the hydrogen donor molecule is in a reaction mediatus comprising the oxygen transferring enzyme and (M1) in the presence of oxygen and incubating under suitable reaction conditions; (2) the enzymatic production (M3) of terminally or subterminally hydroxylated (position omega-1 to omega-4) catty acids comprising; (i) mixing a hydroxylatable fatty acid or fatty acid derivative in the presence of (M1) and oytochrome P450 monooxygenase; and (ii) isolating the hydroxylated product; (3) a monooxygenase; and (11) isolating the hydroxylated fatty acids as described in (2); and (4) detecting (M4) fatty acid-monooxygenases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bioreactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor; electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase.
                  QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM
                                                                                                                           VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
                                                                                                                                           HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV
                                                                                                                                                                                                         B. megaterium cytochrome P450 monooxygenase BM-3 protein.
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        label in (M1); and (ii) qualitatively or quantitatively detecting the signal. The invention is useful for the production of omega-hydroxylated fatty acids and the detection of fatty acid monoxygenases. The invention provides an alternative electron donor system of enzymes with redox properties that is cheaper and more efficient, where the enzyme
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This invention describes a novel modified cytochrome P450 (I) having, as a result of site-specific mutagenesis of its substrate-binding domain, an altered substrate profile, relative to the wild-type, when used for terminal and/or subterminal enzymatic hydroxylation of aliphatic carboxylic acids. The invention also describes (1) nucleic acid (II) candoing (I), and its complement, (2) expression assette (EC) containing (II) and control elements; (3) a vector containing at least one EC; (4) recombinant microorganisms transformed with at least one vector of (3); and (5) enzymatic production of terminally and/or subterminally (3); dydroxylated aliphatic carboxylic acids (A) using the microorganisms of (4), or isolated (I). (I), and recombinant cells that express them, are used to produce hydroxylated aliphatic carboxylic acids or their especially for hydroxylation of 8-12c fatty acids at the omega-1, cand/or 3 positions, and may also have increased reactivity and/or
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                  VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
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                                                                                                                                                                                                                                                                                                                                 B. megaterium cytochrome P450 monooxygenase BM-3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Process for oxidizing acyclic or cyclic terpenes, cycloalkenes, or derivatives for preventing or treating infection in human or animal body comprises mutant haem-containing enzyme which has substitution of amino acid in the active site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a process for oxidizing an acyclic or cyclic terpene, a cycloalkene, or a derivative. The process comprises oxidizing the compound with a mutant haem-containing enzyme which comprises a substitution of an amino acid in the active site by an amino acid with a less polar side-chain. The process is useful for oxidizing an acyclic or cyclic terpene, a cycloalkene, or their derivatives. The process is also useful for product useful for preventing or treating infection in a human or product useful for preventing or treating infection in a human or animal body. The present sequence represents the amino acid sequence of the process of the invention.
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                                              Terpene; cycloalkene; haem-containing enzyme; mutant; oxidation;
infection; P450-BM3.
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Amino acid sequence of the P450-BM3 sequence
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Best Local Similarity 100.0%; Pr
Matches 1048; Conservative 0;
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Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin
                                                                                                                                                                                                                                                               The present sequence represents a cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono- or poly-cyclic aromatic heterocyclics containing nitrogen, sulphur or oxygen, optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkenes. The modified cytochrome P450 monooxygenase are specifically used to oxidize indole to indigo and indorubicin. However, they may be used to oxidize many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRDKTIWGDDVEEFRPERFENDSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH
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has wide substrate
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                                                                                                                                                                                                               P450 monooxygenase for oxidizing for converting indole to indigo,
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100.0%; Pred. No. 0;
11ve 0; Mismatches
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                                                                                                   27-JUL-1999; 99DE-1035115.
18-NOV-1999; 99DE-1055605.
22-MAR-2000; 2000DE-1014085.
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                      Bacillus megaterium
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Matches 1048; Conserv
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           PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP
                                  PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR
                                         DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL
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                                                                                                                                                                                                                                                                                                      sequence of a modified P450 monooxygenase protein.
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Schmid
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                                                                                              GEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNQPKTYVQHVMEQDGKKLI 987
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18-NOV-1999; 99DE-1055605.
22-MAR-2000; 2000DE-1014085.
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                                                     not appear in the specification; it was created
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                                                                                                                                                                                          189 QRANPDDPAYDENKROFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLMGKDPETGEP
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100.0%; Pre
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                                      other substrates.
note: this sequence does no using information provided.
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368 428 428 488 488 548 548 728

728 788 788

608 608 668 668 848 848 908 968 968

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FEGTY EEWREHMWSDVAAY FULDI ENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a modified cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono- or poly-cyclic aromatic heterocyclics containing nitrogen, sulphur or oxygen; optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkanes are specifically used to oxidize indole to indigo and indorublcin. However, they may be used to oxidise many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 KQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this sequence does not appear in the specification; it was created
                                                                                                                                     P450 monooxygenase; oxidization; indole; indigo; indorubicin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organic compounds, useful has wide substrate range
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                                                                                                            Amino acid sequence of a modified P450 monooxygenase protein.
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100.0%; Pred. No. v.
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P450 monooxygenase for oxidizing for converting indole to indigo,
                                                                                                                                                                                                            note- "wild type Ala
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                                                                                                                                                                                                                                     'note- "wild type Phe
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                                     standard; Protein; 1048
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99DE-1055605.
2000DE-1014085.
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                                                                                      (first entry)
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Best Local Similarity 100.
Matches 860; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      B, Pleiss J,
                                                                                                                                                            Bacillus megaterium
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18-NOV-1999;
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                                                                                                                                      Cytochrome
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                                                             AAB31981;
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Li Q;
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using
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HTAFSRMPNOPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020
                                                                                                                                                                                                                                                                                                                                                                            DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL
                                                                                                                                                                                                                     PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR
              EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK
                                                                                                                                                                                                                                                                                                            VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein is a fusion of bovine adrenal cytochrome P450 17-alpha and Bacillus megaterium-derived cytochrome P450 BM-3. The fusion protein has the monoatomic oxygenation activity of the former and the reductivity supplying activity of the latter. Plasmid p(alphaBM1),
                                                    GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG
                                                                                                     661 AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      idase coding gene - has both mono-atomic bovine adrenal cytochrome p450 17-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine adrenal; cytochrome P450; oxidase; reductase; steroid;
plasmid p(alphaBM1).
                                                                                                                                                                                                                                                                                                                                                                                                                               HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P450 17-alpha/P450 BM-3 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxygenation activity of bovine adrand reductivity supplying activity
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                                                                                                                                                                                                The present invention relates to a process for enzymatically oxidising the halogenated aromatic compounds such as 1,2-dichlorobenzene, 1,2,4-trichlorobenzene, 3,3'-dichlorobiphenyl or 2,2',4',5', 5'-fortichlorobenzene, 3,3'-dichlorobiphenyl or 2,2',4',5', 5'-fortichlorobiphenyl. The process comprises treating the polluted environment with a monooxygenase enzyme. A monooxygenase enzyme, P450cam, and its physiological electron transfer partners, putidaredoxin and putidaredoxin reductase, are used to oxidise the halogenated aromatic compounds. Also mutants of the monooxygenase enzyme with substitutions in the active site have enhanced oxidation activity. The process and the transgenic plant or animal which expresses the monooxygenase enzyme are used for detoxifying the environment polluted with the halo aromatic compounds. The present sequence is a Bacillus megaterium monooxygenase enzyme, P450BM-3, which is homologous to the monooxygenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                            environments contaminated with halo treating the affected area with a
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 1049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 846; DB
Pred. No. 0;
0; Mismatches
                                                                                                                                                                            Disclosure; Page 32-39; 42pp; English
                                                                                                                                      aromatic compounds comprises
                                                                                                                                                                                                                                                                                                                                                                                                                            80.7%;
99.8%;
                                     (ISIS-) ISIS INNOVATION LTD.
                                                                                                                            New process for detoxifying
             99GB-0014373
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.8
Matches 1046; Conservative
                                                                                                                                                     monooxygenase enzyme
                                                                                      WPI; 2001-071397/08
                                                                                                                                                                                                                                                                                                                                                                                                   1049 AA;
                                                            Wong LL, Jones JP;
                                                                                                   N-PSDB; AAD02365.
                                                                                                                                                                                                                                                                                                                                                                          enzyme, P450cam.
             18-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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present sequence represents a B. megaterium P-450BM-3 peptide fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA mol. encoding cytochrome P450 oxido:reductase esp. isolated from filamentous fungi, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 693;
                                                                                 Length 17;
                                                                                                                       Indels
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                                                                                 DB 20; I
2.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; L
8.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monooxygenase.
                                                                                 1.6%; Score 17; DB 100.0%; Pred. No. 2.6 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig. 2; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEDE ) NEDERLANDSE ORG TOEGEPAST
                                                                                                                                                                                                                                                                                                              AAR66738 standard; Protein; 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytochrome-P450-oxidoreductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome-P450-oxidoreductase
                                                                                                                                                                  259 ITFLIAGHETTSGLLSF 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus niger ATCC 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB49682 standard; Protein;
                                                                                                                                                                                          1 ITFLIAGHETTSGLLSF
                                                                        Ouery Match
Best Local Similarity 100.C
Matches 17; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van DEN BRINK JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           693 AA;
                                          17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ79914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-1995
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                                            Sequence
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                                                                                                                                                                                                                                                                       RESULT 12
AAR66738
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AAB49682
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                                                                                                                                                                                                                                                                                                                                                        NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides an isolated, mutated Monoamine Oxidase B (MAO B) enzyme having at least one amino acid substitution for wild-type amino acids in a MAO B active site, the wild-type amino acid residues selected from Phe423, Glu427 and Thr428. A plasmid containing the DNA encoding the mutated MAO B and regulatory elements can be used for the recombinant regulation of the enzyme. The mutated MAO B enzyme is useful for indirect regulation of cellular neurotransmitters and vascamines, as the substitutions reduce MAO B's activity and alters its PH profile. The
                                                                                                                                                                                                                                                                     865
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                                                                                                                                                                                                                                                                                                              887
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                                                                                                                                                                                                                                                  YYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSE
                                                                                                                                                                                                                                                                                                                                                                                             FTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQE
                                                                                                                                                                                                                            768 AAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPR
                                                                                                                                                                                          Gaps
  encoding the fusion protein, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation; MAO B; cellular neurotransmitter;
containing the recombinant sequence encoding the fusion protein, is used to transform Saccharomyces cerevisiae. The transformant is designated AH22(p(alphaBM-1)) and can be used for the synthesis of
                                                                                                                                                                                        ö
                                                                                                                                             Length 1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mutant enzyme useful for regulation of neurotransmitters
                                                                                                                                                                                      Indels
                                                                                                                                  Score 266; DB 12; I
Pred. No. 5.9e-260;
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0
                                                                                                                                                          100.0%; Pred. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVEATLMKSYADVHQVSEADARLWLQ 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1046 AVEATLMKSYADVHQVSEADARLWLQ 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY27545 standard; peptide; 17
                                                                                                                                             25.4%;
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                                                                                                                                                                Best Local Similarity 100.
Matches 266; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-561665/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus megaterium
                                                                                                    1085 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vasoamine; enzyme;
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                                                                                                    Sequence
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                                                                                                                                           Query Match
                                                           steroids
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Gaps

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98DE-1014528
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Beauveria bassiana.
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                                      DE19814528-A1
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                                                                                                                                                                                           (BADI ) BASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                    01-APR-1998;
                                                                                                                01-APR-1998;
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                                                                          07-0CT-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to DNA sequence AAF29129 which encodes a human reductase represented in AAB49682. The DNA sequence shows homology with nucleotide sequences of cytochrome p450 reductases and nitric oxide synthases. The protein is related to members of the FNR gamily of synthases. The protein is related to members of the FNR gamily of lavoproteins. This reductase gene maps to human chromosome 9. The reductase polypeptide are useful in screening assays, particularly as diagnostic reagents for detecting abnormally decreased or increased levels of the reductase polypeptide or mRNA expression. In particular, these are useful for diagnosing or determining susceptibility of a subject to a disease associated with altered levels of reductase include cancer, and the sequences may be used in methods for drug bloactivation. The polypeptides and polynucleotides may also be used as vaccines to protect an individual against these diseases. The polypeptide or its fragments are also useful as immunogens to produce antibodies that are immunospecific for the reductase polypeptides. The polypeptide are immunospecific for the reductase polypeptides. The polypeptide are immunospecific for the reductase polypeptides. The polypeptide are immunospecific for the reductase polypeptides. The polyputice and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                    Human; reductase; flavoprotein; cytochrome p450 reductase; chromosome nitric oxide synthase; cancer; drug bioactivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated reductase polypeptides and polynucleotides, useful in screening assays, particularly for diagnosing a disease associated wisltered levels of reductase and as vaccines to protect an individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POPS; 2-phenoxypropionic acid; 2-(4-hydroxyphenoxy) propionic acid; herbicide intermediate; hydroxylation rate; reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 0.00081;
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              Human reductase amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. bassiana POPS reductase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 25-26; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY33673 standard; Protein; 700 AA
                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         against these diseases
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-112221/12.
N-PSDB; AAF29129.
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                              Powell DJ, Tew DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression studies
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                                                                                                                                                WO200077180-A1.
                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                 16-JUN-1999;
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This invention describes a novel method for the production of 2-(4-hydroxyphenoxy) propionic acid (1) from 2-phenoxypropionic acid (POPS) or its sails. The method comprises a microorganism containing at least one of the genes contained within a Beauverial bassiana genomic sequence of 11292 bp (I), with two open reading frames. (I) is useful as a herbicide intermediate. Microorganisms containing multiple copies of (I) have significantly increased hydroxylation rates. This sequence represents the Beauveria bassiana POPS reductase described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytochrome P450 monooxygenase; cytochrome P450 reductase; NPR; pigment production; indole; dye; cosmetic industry; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                Production of 2-(4-hydroxyphenoxy) propionic acid from 2-phenoxypropionic acid using microorganism having increased hydroxylation rate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13; DB 20; Length 700;
Pred. No. 0.00093;
0; Mismatches 0; Indels
   Van Zeijl C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human derived cytochrome P450 reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYQU ) UNIV QUEENSLAND.
(UYVA-) UNIV VANDERBILT.
(CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                           Example 5; Page 28-31; 36pp; German.
   Van Gorcom R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB73901 standard; Protein; 677 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Sco..
100.0%; Pre
0;
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Best Local Similarity 100.
Matches 13; Conservative
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Hauer B, Dingler C,
                                                        WPI; 1999-552253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           700 AA;
                                                                                           N-PSDB; AAZ23663
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DR WPI; 2001-257635/26.

N-PSDB; AAF76960.

XX

PT Generation of genetically modified cell to produce pigment

XX

XX

PT Generation of genetically modified cell to produce pigment

XX

Claim 39; Page 145-148; 178pp; English.

XX

The present sequence is cytochrome P450 reductase. The invention

CC cytochrome P450 sequences. It involves the use of genetic material

CC encoding a cytochrome P450 protein or a functional derivative or

CC chomologue of it in the generation of a genetically modified coll

CC claim has the capacity to produce a pigment in the presence of indole,

CC or a precursor, analogue or derivative of indole, upon expression of

CC the genetic material. Pigment from plant or plant material is useful

CC in the dye or cosmetic industry or as commercial tags or as markers for

XX

Sequence 677 AA;
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Search completed: May 29, 2003, 08:41:38 Job time : 78 secs

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0; Gaps

Query Match
1.1%; Score 12; DB 22; Length 677;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels

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(without alignments)
1063.284 Million cell updates/sec
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1048
1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048
                                                                                                              May 29, 2003, 08:27:11; Search time 29 Seconds
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                            262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1: /cgn2\_6/ptodata/1/laa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/laa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/laa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/laa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*

Issued\_Patents\_AA:\*

## SUMMARIES

		30, Appl		-	4, Appl	4394, Ap	, Appli	3, Appl	1, Appl	3, Appl	, Appli	, Appli	, Appli	1, Appl	, Appli	, Appli	1, Appl			, Appli	, Appli	, Appli	13, Appl	84, Appl	, Appli	2, Appl	, Appli	, Appli
	Description	Sequence 3	Sequence 2			-		Sequence 1	Sequence 1	Sequence 1	Sequence 4	Sequence 5	Sequence 4	Sequence 2	Sequence 4	Sequence 4	Sequence 2	_	_	Sequence 3	Sequence 6	Sequence 3	Sequence 8	Sequence 8	Sequence 5	Sequence 1	Sequence 2	Sequence 2
SOFIES	ΔI	US-09-057-897-30	US-09-265-653-20	US-08-553-279-2	US-09-627-216A-14	US-09-134-001C-4394	US-07-642-002-2	US-08-365-486A-13	US-08-319-866-11	US-08-880-342-13	US-08-705-625-4	US-09-010-998-5	US-09-220-574-4	US-08-365-486A-21	US-09-123-708-4	US-09-123-624-4	US-08-880-342-21	US-08-365-486A-19	US-08-880-342-19	US-08-705-625-3	US-09-010-998-6	US-09-220-574-3	US-09-302-620B-83	US-09-302-620B-84	US-08-147-812-5	US-08-319-866-12	US-09-123-708-2 .	US-09-123-624-2
	В	4	4	-	4	4	-	~	~	4	~	m	4	~	4	4	4	~	4	7	m	4	4	4	-	~	4	4
	Query Match Length DB	20	17	693	588	629	1429	1429	1429	1429	1430	1430	1430	1433	1433	1433	1433	1434	1434			-	619	619	1144	1144	1144	1144
dР	Query Match	1.9	1.6	1.4	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	6.0	6.0	6.0	6.0	6.0	6.0
	Score	20	17	15	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	6	0	6	6	6	6
	Result No.	1	7	m	4	Ŋ	9	7	<b>&amp;</b>	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

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Gaps ö

Query Match
1.9%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels

δ QQ

Patent No. 5212296 Sequence 11, Appl Sequence 25, Appl Sequence 25, Appl Sequence 22, Appl Sequence 12, Appl Sequence 22, Appl Sequence 24, Appl Sequence 9, Appl Sequence 9, Appl Sequence 9, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl		Human
406 6 5212296-6 412 1 US-08-102-863-11 504 1 US-08-457-20865-11 504 1 US-08-457-2048-5 505 4 US-09-627-2168-12 505 4 US-09-126-4208-25 513 4 US-09-126-4208-22 513 4 US-09-126-4208-22 513 4 US-09-126-4208-3 514 0S-08-18-866-9 31 2 US-08-511-872-4 31 2 US-08-511-872-6 31 2 US-08-511-872-10 31 2 US-08-511-872-10 31 3 US-08-511-872-10 31 3 US-08-511-872-11 31 4 US-09-398-173-77	ALIGNMENTS	lication US/09057897  76  Authony Y.H.  Wanthony Y.H.  Wartow: Regina W.  WAITON: Anti-Peptide Antibody Against  WEADRESS: 36  WEADRESS: 36  METCK & CO., Inc.  O. Box 2000  O. Box 2000  ABLE FORM:  I Floppy disk  ISS  CATION DATA:  CATION DATA:  I ON:  WANDER: US/09/057,897  INWERE: US/09/057,897  INWERE: 19902  TION:  I J. Mark  WANDER: 19902  TION:  CATION ON: 30:  ACTERIFICE:
28 8 0.8 3.1 8 0.8 3.2 8 0.8 3.3 8 0.8 3.3 8 0.8 3.3 3.3 8 0.8 3.3 3.4 8 0.8 3.3 3.4 8 0.8 3.4 4.1 7 0.7 4.1 4.2 7 0.7 4.4 4.1 7 0.7 4.4 4.1 7 0.7 4.4 4.1 7 0.7 4.4 4.1 7 0.7 4.4 4.1 7 0.7 4.4 4.1 7 0.7 4.4 4.1 7 0.7 4.4 4.5 7 0.7 4.5 4.5 7 0.7 4.5 4.5 7 0.7 4.5 7 0	· ·	157-897-30 ence 30, App ence 30, App ent No. 63004 EPLICANT: W EPLICANT: W ITLE OF INVE UMBER OF SEQ ORRESPONDENC ADDRESSEE: No. CITY: Rahw STREET: W COUNTRY: U ZIP: READ COUNTRY: U ZIP: APPLICATION COUNTRY: A COUNTRY COUNTRY: A COUNTRY: A COUNTRY: A COUNTRY COUNTRY COUNTRY COUNTR
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Query Match 1.0%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.3 Matches 10; Conservative 0; Mismatches
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100.0%; Pred. No. 0.3
:ive 0; Mismatches
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                      Sequence 14, Application US/09627216A Patent No. 6368837
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Helianthus tuberosus
                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.0
Best Local Similarity 100.
Matches 10; Conservative
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                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08553279
Patent No. 5801024
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: No. 5801024el oxidoreductase from filamentous funghi,
TITLE OF INVENTION: DNA coding therefore and cells transformed with said DNA.
NUMBER OF SEQUENCES: 9
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Amino acid sequence containing conserved site of ; OTHER INFORMATION: Bacillus megaterium P-450BM3 US-09-265-653-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6%; Score 17; DB 4; Length 17; 100.0%; Pred. No. 1.4e-09; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,279
                              Sequence 20, Application US/09265653
Patent No. 6451570
GENERAL INFORMATION:
APPLICANT: Abell: Creed W.
TITLE OF INVENTION: Mutants of Monoamine Oxidase B
FILE REFERENCE: D6048
CURRENT APPLICATION NUMBER: US/09/265,653
CURRENT FILING DATE: 1999-03-10
FALLER APPLICATION NUMBER: US 60/077,482
EARLIER PILING DATE: 1998-03-11
NUMBER OF SEQ ID NOS: 27
FEMALER PILING DATE: 1998-03-11
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: EP PCT/NL94/00135
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 15;
100.0%; Pred. No.
:ive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 ITFLIAGHETTSGLLSF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 693 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.6%
Best Local Similarity 100.0
Matches 17; Conservative
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ses 15; Conservative
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RESULT 2
US-09-265-653-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-553-279-2
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RESULT 5
US-09-134.001C-4394

JUS-09-134.001C-4394

Sequence 4394, Application US/09134001C

Sequence 4394, Application US/09134001C

Sequence 4394, Application US/09134001C

SEQUENCE 6.1000CECT FOR DIABORATION OF TITLE OF INVENTION: WORDER US/09/134,001C

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

WUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4394

LENGTH: 629
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APPLICANT: Sariasiani, Sima F
APPLICANT: Tang, Xiao Song
APPLICANT: Tang, Xiao Song
APPLICANT: Up well well
APPLICANT: Up well well
APPLICANT: Gatenby, Anthony
TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
FILE REFERENCE: BC1009 US NA
CURRENT APPLICATION NUMBER: US/09/627,216A
PRIOR PLICATION DATE: 1999-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 629;
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0.36;
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Patent No. 5268465
GENERAL INFORMATON:
APPLICANT: Bredt, David S.
APPLICANT: HWANG, Paul M.
APPLICANT: Reed, Randall
APPLICANT: Reed, Randall
APPLICANT: Snyder, Solomon H.
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TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 amino acids
                                                                                                                                                                                                                                                                                                              1172 PRYSISSSP 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-319-866-11
                                                                                                                                               , MOLECULE TYPE: protein US-08-365-486A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                       826 PRYSISSSP 835
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                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
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TITLE OF INVENTION: Purification and Molecular Cloning of Nitric TITLE OF INVENTION: Oxide Synthase NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 10; DB 1; Length 1429;
100.0%; Pred. No. 0.79;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 13, Application US/08365486A
patent No. 5814306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
STREET: CA.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,002
FILING DATE: 19910118
CLASSIFICATION: 435
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET UNMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 296-5500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1429 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                     USA
                                                                                                                94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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Gaps
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                                                                                                                                                                                                                                                      Sequence II, Application US/08319866
Patent No. 592923
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tully, Timothy P.
APPLICANT: You's C.
APPLICANT: Regulski, Michael
TITLE OF INVENTION: GLONING AND CHARACTERIZATION OF GENES
TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1429;
  Length 1429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10; DB 2;
Pred. No. 0.79;
Query Match 1.0%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.7 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.0%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.7 Matches 10; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/319,866 FILING DATE: 7-OCT-1994 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFRENCE/DOCKET NUMBER: CSH
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1429 amino acids
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Length 1430;
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APPLICANT: Snyder, Solomon
APPLICANT: Snyder, Solomon
APPLICANT: Jaffrey, Samie
APPLICANT: Snowman, Adele
APPLICANT: Eliasson, Mikael
APPLICANT: Cohen, No. 6103872m
TITLE OF INVENTION: CAPON, a protein that binds
TITLE OF INVENTION: neuronal nitric oxide synthase
NUMBER OF SEQUENCES: 8
CORRESPEDUDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,625
FILING DATE: 30-AUG-1996
CLASSIFICATION: 530
ATTONENY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISCHARION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 31,141
REFERENCE/DOCKET NUMBER: 01107.57071
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
0.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DGS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 10; DB 100.0%; Pred. No. 0.7 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/09/010,998
22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09010998 Patent No. 6103872
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1430 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.0°
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1172 PRYYSISSSP 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                  ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                826 PRYYSISSSP 835
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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STATE: D
COUNTRY:
CITY: Wa
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US-09-010-998-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                  APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Namette H.
APPLICANT: Aurphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Laderoute, Keith R.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10; DB 4; Length 1429; Pred. No. 0.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08705625
Patent No. 5908756
GENERAL INFORMATION:
APPLICANT: Snyder, Solomon H.
APPLICANT: Jaffrey, Samle R.
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BCS/MS-DOS
SOFTWARE: PATENTIN RC-BCS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING APPLICATION 514
PRIOR APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTONINY/AGENT INFORMATION:
AND ATTONINY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.7
Mismatches
                                                    Sequence 13, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEC ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Banner & Witcoff
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          826 PRYYSISSSP 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Gaps

Gaps

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GENERAL INFORMATION:
APPLICANT: SCHRADER, Juergen
APPLICANT: GOEDECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
TITLE OF INVENTION: TREATWENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2003
CURRENT APPLICATION NUMBER: US/09/123,708
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  Indels
                                                                                                                                                                    Sequence 21, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webstor: Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10; DB 2;
Pred. No. 0.79;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      SEE: Dehlinger & Associates
: 350 Cambridge Avenue, Suite 250
Palo Alto
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: P4411402.8
EARLIER FILING DATE: 1994-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: 510-123-4
RATGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-123-708-4
: Sequence 4, Application US/09123708
: Patent No. 6146887
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Best Local Similarity 100.
Matches 10; Conservative
10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                      826 PRYYSISSSP 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   826 PRYYSISSSP 835
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                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
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                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-365-486A-21
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  Matches
                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                             Length 1430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SOUGHON H.
APPLICANT: Jaffrey, Samie R.
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner & Witcoff
STREET: 1001 G Street, N.W.
CIT: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/220,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.0%; Score 10; DB 4; 100.0%; Pred. No. 0.79;
                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                  0.79;
                                                                                                                                                                                                                                                                                                             Ouery Match 1.0%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.7 Matches 10; Conservative 0; Mismatches
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                                      01107.73424
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APPLICATION NUMBER: 08/705,625
FILING DATE: 30-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPHONE: 202-508-929
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09220574
Patent No. 6168926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
              REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-508-9100
TELEFAX: 202-508-929
                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6103872e
US-09-010-998-5
                                                                                                                             INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 1430 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1430 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                    Kagan, Sarah A
                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                           826 PRYYSISSSP 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20001-4597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM:
US-09-220-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-220-574-4
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Gaps

Search completed: May 29, 2003, 08:32:17 Job time : 30 secs

1176 PRYSISSSP 1185

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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 29, 2003, 08:30:56; Search time 54 Seconds (without alignments) 1964.489 Million cell updates/sec Run on:

US-10-031-146-2 1048 1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Title: Perfect score:

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

383519 seqs, 101223694 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
3: /cgn2\_6/ptodata/2/pubpaa/USO6\_NEW\_PUB.pep:\*
4: /cgn2\_6/ptodata/2/pubpaa/USO6\_NEW\_PUB.pep:\*
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7: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
8: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
9: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
10: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/2/pubpaa/USO9\_PUBCOMB.pep:\*
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13: /cgn2\_6/ptodata/2/pubpaa/USO9\_PUBCOMB.pep:\*
13: /cgn2\_6/ptodata/2/pubpaa/USO6\_PUBCOMB.pep:\*
14: /cgn2\_6/ptodata/2/pubpaa/USO6\_PUBCOMB.pep:\* Published\_Applications\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

No.   Score Match Length DB ID   Description			æ				
9 US-10-119-604C-20 Sequence 20, April 10 US-09-778-319-2 Sequence 23, April 23 Sequence 23, April 247-23 Sequence 24, April 247-249-14 Sequence 14, Bril 10 US-09-765-873-14 Sequence 14, Bril 10 US-09-740-046-4 Sequence 14, Bril 210-138-838-83 Sequence 14, Bril 210-138-838-117 Sequence 117, April 247-838-117 Sequence 117, April 247-938-117 Sequence 117, April 247-938-117 Sequence 117, April 247-938-117 Sequence 117, April 247-938-118 Sequence 117, April 247-938-905-84 Sequence 117, April 247-938-905-84 Sequence 117, April 247-938-905-118 Sequence 118, April 247-938-905-905-905-905-905-905-905-905-905-905	Result No.	Score	Query Match	Length	DB	ID	Description
9 US-09-778-319-2 Sequence 2', April 10 US-09-76-873-14 Sequence 2', April 10 US-09-76-873-14 Sequence 14', Bourson 14', B	1	17	1.6	17	١٥	US-10-119-604C-20	Sequence 20, Appl
9 US-09-371-347-23 Sequence 23, 7 Sequence 23, 7 Sequence 24, 9 US-09-224-249-14 Sequence 14, 9 US-09-740-046-4 Sequence 14, 9 US-10-224-249-14 Sequence 14, 9 US-10-138-838-83 Sequence 4, 6 US-10-138-838-11 Sequence 81, 8 US-10-138-838-11 Sequence 117, 9 US-10-139-031-84 Sequence 118, 9 US-10-139-031-11 Sequence 117, 9 US-10-139-031-11 Sequence 117, 9 US-10-138-905-84 Sequence 81, 8 US-10-138-905-84 Sequence 81, 8 US-10-138-905-84 Sequence 81, 8 US-10-138-905-11 Sequence 81, 8 US-10-138-905-11 Sequence 81, 8 US-10-138-905-11 Sequence 117, 9 US-10-138-905-11 Sequence 81, 8 US-10-14 Sequence 81, 8 US-10-14 Sequence 81, 8 US-10-14 Se	7	13	1.2	597	σ	US-09-778-319-2	~
10 US-09-765-873A-14 Sequence 14, 10 US-09-765-873A-14 Sequence 14, 10 US-09-740-046-4 Sequence 4, 11 US-09-740-046-4 Sequence 4, 12 US-10-138-838-84 Sequence 83, 13 US-10-138-838-117 Sequence 81, 13 US-10-138-938-117 Sequence 117, 13 US-10-139-031-84 Sequence 117, 13 US-10-139-031-14 Sequence 118, 13 US-10-139-031-14 Sequence 118, 13 US-10-138-905-84 Sequence 118, 14 US-10-138-905-84 Sequence 118, 15 US-10-138-905-84 Sequence 118, 15 US-10-138-905-84 Sequence 118, 15 US-10-138-905-117 Sequence 118, 15 US-10-138-905-117 Sequence 118, 15 US-10-138-905-117 Sequence 118, 15 US-10-138-905-117 Sequence 81, 18, 18 US-10-138-905-118 Sequence 81, 18 US-10-188-905-118 Sequence 81, 18 US-10-188-905-118 Sequence 81, 18 US-10-188-905-118 Sequence 81, 18 US	m	12	1.1	677	σ	US-09-371-347-23	•
9 US-10-224-249-14 Sequence 14, 10 US-09-70-046-4 Sequence 4, 2 Sequence 4, 2 Sequence 13, 2 US-10-138-838-83 Sequence 83, 2 US-10-138-838-118 Sequence 117, 3 Sequence 117, 3 Sequence 118, 3 Sequence 117, 3 Sequence 118, 3 Sequence 84, 8 US-10-138-905-83 Sequence 84, 8 US-10-138-905-118 Sequence 117, 9 US-10-138-905-118 Sequence 117, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-905-118 Sequence 83, 8	4	10	1.0	588	10	US-09-765-873A-14	
10 US-09-740-046-4 Sequence 4, P. 9 US-10-138-818-83 Sequence 83, P. 9 US-10-138-818-84 Sequence 81, P. 9 US-10-138-818-117 Sequence 117, P. 9 US-10-138-818-118 Sequence 118, P. 10-139-031-84 Sequence 118, P. 10-139-031-117 Sequence 117, P. 10-139-031-118 Sequence 117, P. 10-138-905-83 Sequence 84, P. 10-138-905-83 Sequence 84, P. 10-138-905-84 Sequence 117, P. 10-138-905-84 Sequence 117, P. 10-138-905-84 Sequence 117, P. 10-138-905-84 Sequence 117, P. 10-138-905-84 Sequence 118, P. 10-138-905-118 Sequence 84, P. 10-138-905-118 Sequence 81, P. 10-138-905-118 Sequence 83, P. 10-10-138-905-118 Sequence 83, P. 10-10-138-916-83 Sequence 83, P. 10-10-138-916-818, P. 10-10-10-10-10-10-10-10-10-10-10-10-10-	S	10	1.0	1433	σ	US-10-224-249-14	: ``
9 US-10-138-838-83 Sequence 83, p. 9 US-10-138-838-834 Sequence 81, p. 9 US-10-138-838-117 Sequence 117, p. 9 US-10-138-838-118 Sequence 118, p. 9 US-10-139-031-84 Sequence 118, p. 9 US-10-139-031-117 Sequence 118, p. 9 US-10-139-905-83 Sequence 118, p. 9 US-10-138-905-84 Sequence 118, p. 9 US-10-138-905-117 Sequence 118, p. 9 US-10-138-905-117 Sequence 118, p. 9 US-10-138-905-118 Sequence 83, p. 9 US-10-138-916-83 Sequence 83, p. 9 US-10-138-916-818, p. 9 US	9	6	6.0	516	10	US-09-740-046-4	Sequence 4, Appl
9 US-10-138-838-84 Sequence 84, P. 9 US-10-138-838-117 Sequence 117, 2 US-10-138-838-118 Sequence 118, 9 US-10-139-031-83 Sequence 81, P. 9 US-10-139-031-84 Sequence 81, P. 9 US-10-139-031-118 Sequence 117, 9 US-10-138-905-83 Sequence 81, P. 9 US-10-138-905-84 Sequence 81, P. 9 US-10-138-905-117 Sequence 81, P. 9 US-10-138-905-118 Sequence 118, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-905-118 Sequence 81, P. 9 US-10-138-916-83 Sequence 81, P. 9 US-10-138-916-81 Sequence 81, P. 9 US-10-13	7	0	0.9	679	σ	US-10-138-838-83	
9 US-10-138-838-117 Sequence 117, 9 US-10-138-838-118 Sequence 118, 9 US-10-139-031-83 Sequence 118, 9 US-10-139-031-84 Sequence 83, P US-10-139-031-117 Sequence 117, 9 US-10-138-905-83 Sequence 81, P US-10-138-905-84 Sequence 84, P US-10-138-905-117 Sequence 84, P US-10-138-905-117 Sequence 117, 9 US-10-138-905-118 Sequence 117, 9 US-10-138-905-118 Sequence 118, P US-10-138-905-118 Sequence 83, P US-10-118-905-118 Sequence 8	ω	σ	0.9	619	6	US-10-138-838-84	
9 US-10-138-838-118 Sequence 118, 9 US-10-139-031-83 Sequence 83, 8 US-10-139-031-117 Sequence 117, 9 US-10-139-031-118 Sequence 117, 9 US-10-138-905-83 Sequence 118, 9 US-10-138-905-84 Sequence 84, 8 US-10-138-905-117 Sequence 117, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-905-118	6	o	0.9	619	6	US-10-138-838-117	,
9 US-10-139-031-83 Sequence 83, 9 US-10-139-031-84 Sequence 84, 9 US-10-139-031-117 Sequence 117, 9 US-10-139-905-83 Sequence 118, 9 US-10-138-905-84 Sequence 81, 9 US-10-138-905-117 Sequence 81, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-916-83 Sequence 83, 9 US-10-138-916-83 Sequence 83, 8	10	6	0.9	619	6	US-10-138-838-118	118,
9 US-10-139-031-84 Sequence 84, 9 US-10-139-031-117 Sequence 117, 9 US-10-139-031-118 Sequence 118, 9 US-10-138-905-83 Sequence 84, 9 US-10-138-905-117 Sequence 84, 9 US-10-138-905-117 Sequence 117, 9 US-10-138-905-118 Sequence 117, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-916-83	11	6	0.9	619	σ	US-10-139-031-83	83, A
9 US-10-139-031-117 Sequence 117, 9 US-10-139-031-118 Sequence 118, 9 US-10-138-905-83 Sequence 83, 9 US-10-138-905-84 Sequence 84, 9 US-10-138-905-117 Sequence 117, 9 US-10-138-905-117 Sequence 117, 9 US-10-138-916-83 Sequence 118, 9 US-10-138-916-83	12	6	0.9	619	6	US-10-139-031-84	84,
9 US-10-139-031-118 Sequence 118, 9 US-10-138-905-83 Sequence 83, 9 US-10-138-905-84 Sequence 117, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-916-83 Sequence 83,	13	σ	6.0	619	6	US-10-139-031-117	117,
9 US-10-138-905-83 Sequence 83, 9 US-10-138-905-84 Sequence 84, 9 US-10-138-905-117 Sequence 117, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-916-83 Sequence 83,	. 14	6	6.0	619	σ	US-10-139-031-118	118,
9 US-10-138-905-84 Sequence 84, 9 US-10-138-905-117 Sequence 117, 9 US-10-138-905-118 Sequence 118, 9 US-10-138-916-83 Sequence 81,	15	σ	6.0	619	6	US-10-138-905-83	83,
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9 US-10-138-905-118 Sequence 118, 9 US-10-138-916-83 Sequence 83,	17	σ	6.0	619	σ	US-10-138-905-117	117,
9 US-10-138-916-83 Sequence 83, A	18	6	6.0	619	6	US-10-138-905-118	118,
	19	6	0.9	619	0	US-10-138-916-83	83, A

Sequence 84, Appl Sequence 117, App Sequence 118, App Sequence 81, Appl Sequence 117, App Sequence 117, App Sequence 117, App Sequence 114, Appl Sequence 12, Appl Sequence 45, Appl Sequence 45, Appl Sequence 46, Appl Sequence 46, Appl Sequence 22, Appl Sequence 46, Appl Sequence 41, Appl Sequence 41, Appl Sequence 42, Appl Sequence 42, Appl Sequence 41, Appl Sequence 42, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 41, Appl Sequence 42, Appl Sequence 43, Appl Sequence 41, Appl Sequence 41, Appl Sequence 21, Appl Sequence 214, Appl Sequence 214
9 US-10-138-916-84 9 US-10-138-916-118 9 US-09-976-800-83 9 US-09-976-800-117 9 US-09-976-800-117 9 US-09-976-800-117 10 US-09-976-800-118 10 US-09-976-800-118 10 US-09-911-781-11 10 US-09-814-122-43 10 US-09-854-122-43 10 US-09-854-122-45 10 US-09-854-122-45 10 US-09-854-122-45 10 US-09-817-347-48 9 US-09-371-347-48 9 US-09-371-347-44 9 US-09-384-245-214
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# ALIGNMENTS

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                     APPLICANT: Abell, Creed W.
APPLICANT: Lewis, Duane A.
TITLE OF INVENTION: MUTAINES of Monoamine Oxidase B.
FILE REFERENCE: D6048/D
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 09/265,653
PRIOR RILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 27
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.6%; Score 17; DB 9; La
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 17; Conservative 0; Mismatches 0;
                    Sequence 20, Application US/10119604C Publication No. US20030082772A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus megaterium FEATURE:
US-10-119-604C-20
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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Sequence 2, Application US/09778319
Patent No. US20020155560A1
GENERAL INFORMATION.
APPLICANT: POWELL, DAVID J.
APPLICANT: TEW, DAVID G.
TITLE OF INFUNTION: A REDUCTASE
FILE REFERENCE: GH-7667-C1
CURRENT APPLICATION NUMBER: US/09/778,319 259 ITFLIAGHETTSGLLSF 275 1 ITFLIAGHETTSGLLSF 17 US-09-778-319-2 δ g

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Ouery Match 1.0
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                               826 PRYSISSSP 835
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APPLICANT: EXELIXI
     US-09-765-873A-14
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US-09-740-046-4
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Publication No. US20030082676A1

GENERAL INFORMATION:

APPLICANT: BOY A GIAVEL et al.

TITLE OF INVENTION: CLONINO, AND METHODS FOR EVALUATING RISK OF NEURAL TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER

FILE REFERENCE: 50004/003003

CURRENT APPLICATION NUMBER: 05/09/371,347

PRIOR FILING DATE: 1999-01-16

PRIOR FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FASTEED for Windows Version 4.0
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Fatent No. US20010053847A1
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION:
ELIC REFERENCE: BC1009 US CIP
CURRENT APPLICATION NUMBER: US/09/765,873A
CURRENT FILING DATE: 2001-01-19
PRIOR PLILING DATE: 2001-01-19
PRIOR PLILING DATE: 2000-07-27
PRIOR PLILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR PLICATION NUMBER: US 60/147,719
PRIOR PLICATION NUMBER: US 60/147,719
PRIOR PLICATION NUMBER: US 60/147,719
SPIOR APPLICATION OF 38
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 588
                                                                                                                                                                                                                                                                                          Query Match 1.2%; Score 13; DB 9; Length 597; Best Local Similarity 100.0%; Pred. No. 0.001; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%; Score 12; DB 9; Length 677; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 12; Conservative 0; Mismatches 0; Indels
CURRENT FILING DATE: 2001-02-07
PAROR APPLICATION NUMBER: 09/334,490
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 597
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                                                                                                                                                                                                                                                                                                                                                                                                  899 IMVGPGTGVAPFR 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 IMVGPGTGVAPFR 466
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                                                                                                                                                                                                             ; ORGANISM: HOMO SAPIENS ' US-09-778-319-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-371-347-23
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LENGTH: 677
                                                                                                                                                                                     TYPE: PRT
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APPLICANT: Tang, Marian
APPLICANT: Tang, Marian
APPLICANT: Toper, John C.
APPLICANT: Loper, John C.
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REPERBENCE: 1010-16
CURRENT APPLICATION NUMBER: US/09/976,800
PRIOR PILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
SOFTWARE: PETENTIN OF SEQ 118
SOFTWARE: PETENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                      Gaps
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TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO FILE REFERENCE: 1010-16 CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: US/09/976,800
SRIOR FILING DATE: 105/01-012
SOFTWARE: PAtentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 679;
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                                                                                                                                                                                                                                                                                                                                    0; Indels
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Pred. No. 8;
0; Mismatches
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Publication No. US20030049821A1
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100.0%; Pre
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100.0%; Pre
0;
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Cornett, Cathy A.
Brenner, Alfred A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-138-838-117
                                                                                                                                                                                                                                ; ORGANISM: CANDIDATROPICALIS
US-10-138-838-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
                                                                                                                                                                                                                                                                                           Query Match 0.9
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
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                                                                                                                                                                    SEQ ID NO 84
                                                                                                                                                                                                             TYPE: PRT
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APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CTYCCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: CTYCCHROME P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF FITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
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TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXXLAM
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100.0%; Pred. No. c,
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Best Local Similarity 100.0%; Pred. No. 6.2
Matches 9; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
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Publication No. US20030049821A1
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Publication No. US20030049821A1
                     ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-740-046-4
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Madduri, Krishna M.
Cornett, Cathy A.
Brenner, Alfred A.
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Cornett, Cathy A.
Brenner, Alfred A.
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SOFTWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 679
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; ORGANISM: CANDIDATROPICALIS
US-10-138-838-83
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APPLICANT: Craft, David L.
APPLICANT: Elrich, Dudley
APPLICANT: Eshoo, Mark
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APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
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Matches 9; Conservative
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LENGTH: 516
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APPLICANT:
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APPLICANT: LOPEY, John C.
APPLICANT: LOPEY, John C.
APPLICANT: LOPEY, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: PA50 OXIDOREDUCRASE
TITLE OF INVENTION: GENES AND PROTEINS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,031
PRIOR PRILING DATE: 2002-05-03
PRIOR PELING DATE: 2001-0-12
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APPLICANT: GLESSON, MARLIN
TITLE OF INVENTION: CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
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Publication No. US20030049822A1
GENERAL INFORMATION:
                                           Application US/10139031
                                                                                                                                                                                            Madduri, Krishna M.
Cornett, Cathy A.
Brenner, Alfred A.
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Cornett, Cathy A.
Brenner, Alfred A.
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SOFTWARE: Patentin version 3.1
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SOFTWARE: Patentin version 3.1
SEQ ID NO 117
LENGTH: 679
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US-10-139-031-84
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
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APPLICANT: Craft, David L.
APPLICANT: Elrich, Dudley
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Tang, Maria
                                        Sequence 84, Applicat Publication No. US200 GENERAL INFORMATION:
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LENGTH: 679
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                                                    APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROWE
TITLE OF INVENTION: CYTOCHROME P450 OXIDOREDUCTASE
TITLE OF INVENTION: TROPICALIS AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138, 838
FRICR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-10-12
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TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDGCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
CURRENT APPLICATION NUMBER: US/10/139,031
CURRENT FILLIG DATE: 2002-55-03
PRIOR PAPLICATION NUMBER: US/09/976,800
PRIOR FILLING DATE: 2001-10-12
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100.0%; Pre
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APPLICANT: Craft, David L.
APPLICANT: Effich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Madduri, Krishna M.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
Madduri, Krishna M.
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SOFTWARE: Patentin version 3.1
SEQ ID NO 118
LENGTH: 679
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 83
                    Cornett, Cathy A.
Brenner, Alfred A.
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: CANDIDATROPICALIS
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US-10-139-031-83
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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Query Match 0.9%; Score 9; DB 5
Best Local Similarity 100.0%; Pred. No. 8;
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Job time : 54 secs
                         NUMBER OF SEQ ID NOS: 118
SOFWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 679
        PRIOR FILING DATE: 2001-10-12
                                                                                                        ; TYPE: PRT; ORGANISM: CANDIDATROPICALIS
US-10-138-905-83
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APPLICANT: LOPEY. John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
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TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
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    0.9%; Score 9; DB 9;
100.0%; Pred. No. 8;
tive 0; Mismatches
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100.0%; Pred. No. 8;
tive 0; Mismatches
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 118
LENGTH: 679
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                                                                                                                                                                                                                          Sequence 118, Application US/10139031
Publication No. US20030049822A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
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Publication No. US20030068800A1
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
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Cornett, Cathy A.
Brenner, Alfred A.
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Cornett, Cathy A.
Brenner, Alfred A.
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US-10-139-031-118
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Best Local Similarity 100.
Matches 9; Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model Run on:

May 29, 2003, 08:28:41; Search time 297 Seconds

(without alignments)
2275.018 Million cell updates/sec

US-10-031-146-2

Perfect score:

1048 1 TIKEMPOPKIFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

4569144 segs, 644733110 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/1/paa/US60\_COMB.pep:

	Description	Sequence 2, Appli	Sequence 35, Appl	Sequence 2, Appl1	Sequence 2, Appli	Sequence 53927, A	Sequence 9, Appli
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# ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: HAUBER, Bernhard
APPLICANT: HAUBER, Bernhard
APPLICANT: SCHWANEBERG, Ulrich
APPLICANT: SCHWANED CONTINE CONT
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RESULT 2 US-10-031-241-35

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Sequence 35, Application US/10031241
; GENERAL INFORMATION:
   APPLICANT: Hauer, Bernhard
   APPLICANT: Schmid, Rolf D.
   APPLICANT: Schwaneberg, Ulrich
   TITLE OF INVENTION: Electron donor system for enzy
   TITLE OF INVENTION: Conversion of substrates
   FILE REFERENCE: M/40076
   CURRENT APPLICATION NUMBER: US/10/031,241
   CURRENT FILING DATE: 2002-05-06
   PRIOR APPLICATION NUMBER: PCT/EP00/07251
   NUMBER OF SEQ. ID NOS: 35
   SOFTWARE: PatentIn Ver. 2.1
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	1021 HQVSEADARLWLQQLEEKGRYAKDVWAG 1048	PPLICANT: Galva. Declinated by Jurgen PPLICANT: Schwaneberg, Ulrich ITLE OF INVESTION WOMBER: US/10/031,695 ILLE REFERENCE: M/40434 ILLE APPLICATION WUMBER: US/10/031,695 RIOR APPLICATION WUMBER: PCT/EP00/07252 RIOR APPLICATION WUMBER: PCT/EP00/07252 ILLENG DATE: 2000-07-27 ICHERCH: 1048 ILLENG DATE: 2000-07-27 ICHERCH: 1048 ILLENGTH: 1048 ILLENGTH: MARCHIN WEI. Z.1 ILLENGTH: MARCHIN WEI. Z.1 ICHERCH: MARCHIN WEILER WEILER WORTHIN WEILER WARRER WEILER	Score 1048; DB 24; Length 1048; Pred. No. 0; 0; Mismatches 0; Indels 0; Gaps LATDRPVQALMKIADELGEIFKFFAPGRVTRYLSSORLIKE	181 LDEAMNKLQRANPDPRAYDENKRQFOEDIKVMNDLVDKIIARRASGEGSDDLLTHMLNG 240  181 LDEAMNKLQRANPDPRAYDENKRQFQEDIKVMNDLVDKIIADRRASGEGSDDLLTHMLNG 240  181 LDEAMNKLQRANPDPAYDENKRQFQEDIKVMNDLVDKIIADRRASGEQSDDLLTHMLNG 240  241 KDPETGEPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQRAAEBAARVLVD 300  1111111111111111111111111111111111

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APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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601 GEADASDDFEGTYEEWREHWWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG [	Qy 781 EALLEKQAYKEQYLAKRITMLELLEKYPACEMKFSEFIALLPSIRPRYSISSSRRVDEK 840	Db   902 VGPGTGVAPPRGFVQARKQLKEQGOSLGEAHLYFGCRSPHEDYLYGEELENAQSEGIITL   961	ESULT 6 S-10-031-146-9 Sequence 9, Application US/10031146 Septence 9, Application US/10031146 SPELICANT: HAUER, Bernhard APPLICANT: PLEISS, Juergen APPLICANT: SCHWANEBERG, Ulrich APPLICANT: SCHWANEBERG, Ulrich APPLICANT: SCHWANEBERG, Ulrich TITLE OF INVENTION: Novel cytochrome P450 m	FILE REFERENCE: 50915 CURRENT APPLICATION NUMBER: US/10/031,146 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: PCT/EP 00/07253 PRIOR RILING DATE: 2000-07-27 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Word Perfect version 6.1 SEQ ID NO 9	LENGTH: 1049 TYPE: PRT ORGANISM: Bacillus med	Query Match 100.0%; Score 1048; DB 24; Length 1049; Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Ov 1 TIKENDORGREGIANIDIANT DEVANTABLE CETEFORM DEVANTAGE 60	11111111111111111111111111111111111111

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                                                                TYPE: PRT
ORGANISM: Bacillus megaterium
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P14779
DATABASE ENTRY DATE: 1990-04-01
RELEYANT RESIDUES: (1)..(1049)
                                                                                                                                                              0; Mismatches
                                                                                                                                          Query Match 100.0%; Score 1048; Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/340,602
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                        LENGTH: 1049
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APPLICANT: Farinas, Edgardo
APPLICANT: Glieder, Anton
APPLICANT: Arnold, Frances
APPLICANT: Schwanberg, Ulrich
TITLE OF INVENTION: INPROVED CYTOCHROME P450 OXYGENASES
FILE REFERENCE: 3369/JK238-US.
CURRENT APPLICATION UNMER: US/10/201,213
CURRENT APPLICATION DATE: 2002-07-22
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DATABASE ACCESSION NUMBER: Genbank / P14779
DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(1049)
US-10-201-213-2
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PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/308,429
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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Matches 1048; Conservative
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   ; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(1049)
; OTHER INFORMATION: Coding
US-09-856-339A-21
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APPLICANT: Bell, Stephen
APPLICANT: Bell, Stephen
APPLICANT: Bell, Stephen
APPLICANT: Carmicheal, Angus
APPLICANT: Carmicheal, Angus
FILE REFERENCE: HO-P02196US0 (10104571)
CURRENT APPLICATION WUMBER: US/09/886,339A
CURRENT FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: PCT/GB99/03873
PRIOR FILING DATE: 1999-11-19
NUMBER: OF SEQ ID NOS: 23
SEQ ID NO 21
LENTING DATE: 1049
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US-09-856-339A-21
Sequence 21, Application US/09856339A
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ORGANISM: Bacillus
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SEGUERAL INFORMATION:
APPLICANT: Bionomix, Inc.,
APPLICANT: Debe, Derek
APPLICANT: Denser, Joseph
TITLE OF INVENTION: WETHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNDMER: US/09/791,537
CURRENT APPLICATION UNDMER: US/09/791,537
CURRENT APPLICATION UNDMER: DEDITE: SOTOURDER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 94076
LENGTH: 471
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Best Local Similarity
Matches 471; Conserv
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US-09-791-537-94076
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APPLICANT: Luet, Wong
APPLICANT: Jonathan, Jones
TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS
FILE REFERENCE: P02351051 / 10112404 / N.76277B
CURRENT APPLICATION NUMBER: US/10/018,730A
CURRENT PILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SED ID NO 4
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Pred. No. 0;
0; Mismatches
                                                               HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
                                                                            Sequence 4, Application US/10018730A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Bacillus megaterium
US-10-018-730A-4
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Best Local Similarity 99.8%;
Matches 1046; Conservative
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APPLICANT: CITION. PARTICK C.
APPLICANT: CITION. PARTICK C.
APPLICANT: Arnold, Frances H.
TITLE OF INVENTION PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS:
FILE REFERENCE: 4059/IA237-US3
CURRENT APPLICATION NUMBER: US/10/125,640
CURRENT APPLICATION NUMBER: 60/284,215
PRIOR APPLICATION NUMBER: 60/284,215
PRIOR APPLICATION NUMBER: 60/284,636
PRIOR PILING DATE: 2001-04-16
PRIOR PAPLICATION NUMBER: 60/340,602
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P14779
DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(464)
                                                                                                                                                                                                      ; Sequence 3, Application US/10125640; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 464
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                                                       PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQL 360
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APPLICANT: Cirino, Patrick C.
APPLICANT: Cirino, Patrick C.
TITLE OF INVENTION PERCOLIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
FILE REFERENCE: 4059/2X237-W00
CURRENT PAPLICATION NUMBER: PCT/US02/11954
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/284,215
PRIOR PILING DATE: 2001-04-16
PRIOR PILING DATE: 2001-05-03
PRIOR PILING DATE: 2001-15-12
PRIOR PILING DATE: 2001-12-12
SOFTWARE: PATENTING DATE: 2001-12-12
SOFTWARE: PATENTING DATE: 3001-12-12
SOFTWARE: PATENTING DATE: 3001-12-12
SOFTWARE: PATENTING DATE: 3001-12-12
SOFTWARE: PATENTING DATE: 2001-12-12
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DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(464)
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                                                                                                                                                                                                                                                                                                                    Sequence 3, Application PC/TUS0211954 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Bacillus megaterium PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 463; Conservative
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Length 455; Indels

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61 ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMV 120
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                                                                                                                                                                                     1 TIKEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
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                                                                                                                                                       0; Mismatches
                                                                                                                          Query Match 43.4%; Score 455; Best Local Similarity 100.0%; Pred. No. Matches 455; Conservative 0; Mismatch
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he : 301 secs
SOFTWARE: Patentin version 3.0 FROM NO 9264
                                                                              ; ORGANISM: pdb 2BMHA
US-09-791-537-8264
                                                 LENGTH: 455
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                                                                                  Sequence 116499, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Dancer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 116499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8264, Application US/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Biolomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERBENCE: 261-210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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    FDFEDHTNYELDIKETLILKPEGFVVKAKSKKIPLGGIPSPST
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                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 458; Conservative
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; ORGANISM: pdb 1BVYA
US-09-791-537-116499
                                                                             US-09-791-537-116499
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1048
1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048
                                                                                                             May 29, 2003, 08:29:06; Search time 105 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Perfect score:
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Post-processing: Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database: Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/paa/USOS\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/paa/USOS\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/paa/USOS\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/USOS\_NEW\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/paa/USOS\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa/USOS\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	811	Sequence 2518, Ap		763	24, Ap	Sequence 14954, A			Sequence 23, Appl		Sequence 187294,		Sequence 9867, Ap	14, Ap	14,	4394	70174,	23982,			Sequence 8116, Ap	Sequence 8116, Ap	Sequence 2, Appli	Sequence 1, Appli	Sequence 13060, A
DI	-10-156-761	US-10-369-493-2518 US-10-369-493-2517	-10-369-493	US-10-369-493-7634	0-214-446	-10		0-440-	-148-9	US-10-369-493-22034	10-4	US-10-424-599-191313	US-10-156-761-9867	US-10-188-523B-14	0-188-5230	_	US-10-425-114-70174	60-452-680-2	US-60-453-135-14960	-453-050-1	US-60-455-444-8116	US-60-465-241-8116	US-09-661-258-2	- 60	US-09-675-784A-13060
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Score	17	9 -	15	15	15	12	12	12	12	12	11	11	11	10	10	10	10	10	10	10	10	10	10	10	6
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Sequence 47717, A Sequence 44757, A Sequence 3240, Ap	Sequence 3240, Ap Sequence 52887, A Sequence 2, Appli	່ຕໍ່ຕໍ່	11,	83,	Sequence 117, App Sequence 118, App	Sequence 4154, Ap		Sequence 14077, A
US-10-425-114-47717 US-10-425-114-44757 PCT-US02-40225-3240	US-10-320-797-3240 US-10-425-114-52887 US-10-272-017A-2	US-10-272-017A-3 US-10-272-017A-5	US-10-272-017A-6 US-10-400-902-11	US-10-405-660-83 US-10-405-660-84	US-10-405-660-117	US-10-369-493-4154 US-09-751-708A-124	US-09-661-258-5	US-10-219-051B-14077
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27 28 29	30 31 32	333	35 36	37	39	4 4 2	64.	45

### ALIGNMENTS

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APPLICANT: Cac, Yongwei
APPLICANT: Cac, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
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100.0%; Pred. No. 9.3e-08;
tive 0; Mismatches 0; Indels
                                                                                                                                                                 APPLICANT: SHIBA, TADAYCSHI
APPLICANT: SHIBA, TADAYCSHI
APPLICANT: HATTORI, MASHIRA
FILE REFERENCE: 249-262
CURRENT APPLICATION NOWBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/20/204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
FROM FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2518, Application US/10369493 GENERAL INFORMATION:
                  Sequence 8117, Application US/10156761 GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptomyces avermitilis US-10-156-761-8117
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APPLICANT: HORIKAWA, HIROSHI
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Best Local Similarity 100.0
Matches 17; Conservative
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US-10-156-761-8117
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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APPLICANT: Weller, David
APPLICANT: Burk, Mark J.
APPLICANT: Hitchman, Tim
APPLICANT: Hitchman, Tim
APPLICANT: Hitchman, Tim
APPLICANT: Pujol, Catherine
APPLICANT: Pholol, Catherine
APPLICANT: Short, Jay M.
TITLE OF INVENTION: THEM AND METHODS OF MAKING AND USING THEM
TITLE OF INVENTION: THEM AND METHODS OF MAKING AND USING THEM
FILLE REFERENCE: 0910-500001
CURRENT APPLICATION NUMBER: US 60/309,497
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 24
LENGTH: 1077
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1.1e-05;
  Query Match
1.4%; Score 15; DB 6; Length 592;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.4%; Score 15; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                               Sequence 7634, Application US/10369493 GENERAL INFORMATION:
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US-10-369-493-7634
                                                                                                               899 IMVGPGTGVAPFRGF 913
                                                                                                                                              449 IMVGPGTGVAPFRGF 463
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                                                                                                                                                                                                                                             RESULT 5
US-10-369-493-7634
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LENGTH: 592
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Sequence 2517, Application US/10369493

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Clac, Yongwei
APPLICANT: Glater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Glomen, Barry S.
APPLICANT: Glomen, Barry S.
APPLICANT: Glowerion: Expression of MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: Expression of MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2517
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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1.5%; Score 16; DB 6; Length 659;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 16; DB 6; Length 678; 100.0%; Pred. No. 6.4e-07; Live 0; Mismatches .0; Indels
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2518
LENGTH: 659
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                                                                                                                                      ; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Schizosaccharomyces pombe US-10-369-493-2517
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ORGANISM: Burkholderia fungorum
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Best Local Similarity 100.(
Matches 16; Conservative
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SEQ ID NO 4874
LENGTH: 592
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493
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                                                                                                             APPLICANT: NADLER, STEVEN G.
APPLICANT: CARMAN, JULIE
TITLE OF INVENTION: POLYDED AND POLYPEPTIDES ASSOCIATED WITH THE
TITLE OF INVENTION: NF-KB PATHWAY
FILE REFERENCE: 3053-4191
CURRENT APPLICATION NUMBER: US/60/440,068
CURRENT APPLICATION NUMBER: 2063-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: PATENTIN VET. 2.1
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US-10-148-907A-23
; Sequence 23, Application US/10148907A
; GENERAL INFORMATION:
; APPLICANT: Novartis AG
; TITLE OF INVENTION: Compositions and Methods for Halegenation Reactions; FILE REFERENCE: 3-31082B: US/10/148,907A
; CURRENT APPLICATION NUMBER: US/02-06-04
; PRIOR PPLICATION NUMBER: US 60/228801
; PRIOR APPLICATION NUMBER: US 60/219343
; PRIOR FILING DATE: 1999-12-15
; PRIOR FILING DATE: 2000-01-03
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100.0%; Pred. No. 0.0084;
Live 0; Mismatches 0; Indels
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Pred. No.
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                                                                       Sequence 572, Application US/60440068
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1.1%; So
Best Local Similarity 100.0%; P.
Matches 12; Conservative 0;
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 682
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Matches 12; Conservative
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US-60-440-068-572
                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          SEQ ID NO 572
LENGTH: 677
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TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: LeA 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR APPLICATION NUMBER: US 60/3146,382
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SEC ID NO 12757
LENGTH: 676
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Pred. No. 0.0063;
0; Mismatches 0
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US-10-219-051B-12757
                                                                                                                                                   APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
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                                                                                                             Sequence 14954, Application US/10156761 GENERAL INFORMATION:
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-14954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.1%; Scc
Best Local Similarity 100.0%; Pi
Matches 12; Conservative 0;
266 TFLIAGHETTSGLLS 280
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SEQ ID NO 14954
LENGTH: 504
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US-10-219-051B-12757
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TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REPERENCE: BC1009 US DIVCIP
CURRENT APPLICATION NUMBER: US/10/188,523B
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 11; DB 6; Length 1352; llarity 100.0%; Pred. No. 0.17; Conservative 0; Mismatches 0; Indels
                                                           Length 691;
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                                                                                               Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14776C.1.pep
US-10-424-599-191313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                         DB 6;
0.092;
                                                                                                                                                                                                                                                                                                                                            APPLICANT: ISHLKHAN, DANUN
APPLICANT: ISHLKHAN, HIROSHI
APPLICANT: HORKKHAN, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: NUNENTING
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEO ID NOS: 15109
SEO ID NO 9867
LENGTH: 1352
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                                                                                               0; Mismatches
                                                         1.0%; Score 11;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                        Sequence 9867, Application US/10156761 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 588
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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Matches 11; Conserva
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US-10-188-523B-14
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US-10-424-599-187294
Sequence 187294, Application US/10424599
Sequence 187294, Application US/10424599
APPLICANT: La Rosa Thomas J
APPLICANT: A Royalic David K
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
SEQ ID NO 187294
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MUMBER OF SEQ ID NOS: 285684
SEQ ID NO 187294
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Avail: David K
APPLICANT: Avail: David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFREENCE: 38-21(53233)B
CURRENT APLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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LENGTH: 691
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US-10-424-599-187294
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0.0086;
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Pred. No.
                PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22034
LENGTH: 691
                                                                                                                                      ORGANISM: Saccharomyces cerevisiae US-10-369-493-22034
    2003-02-28
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100.0%;
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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US-10-424-599-191313
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 29, 2003, 08:37:32; Search time 99 Seconds (without alignments) 2181,186 Million cell updates/sec Run on:

US-10-031-146-2 1048 1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

671580 segs, 206047115 residues Searched:

0 Word size :

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SPTREMBL\_21:\* Database :

sp\_human: \*
sp\_human: \*
sp\_novertebrate: \*
sp\_mammal: \*
sp\_norganelle: \*
sp\_plage: \*
sp\_plant: \*
sp\_rodent: \*
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sp\_bacteria:\*
sp\_fungi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

## SUMMARIES

Description	Q9ae23 bacillus me	Q8x1w0 coriolus ve	Q00141 asperdillus	O9hq14 phanerochae	09hdq2 phanerochae	094613 schizosacch	Q9uhb4 homo sapien	Q96bc6 homo sapien	032214 bacillus su	Q9kf76 bacillus ha	Q9p4el cunninghame	Q9hfv3 rhizopus st	Q9p4e2 cunninghame	Q9y8g7 fusarium ox	Q9rd76 streptomyce	Q8r0y3 mus musculu
Ð	Q9AE23	Q8X1W0	000141	Q9HG14	Q9HDG2	094613	090нв4	Q96BC6	6 032214	6 Q9KF76	Q9P4E1	Q9HFV3	Q9P4E2	Q9Y8G7	6 Q9RD76	1 Q8R0Y3
% Query Match Length DB	29 2	730 3	. 693	690 3	736 3	558 3	597 4	597 4	605 1	1 209	629 3	671 3	710 3	1066 3	527 1	696
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# ALIGNMENTS

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	PRT; 29 AA.	Created) .	Last sequence update)	(IIEMBLIEI, I/, Last annotation update) 450BM-3 (Fragment).		Bacillus/Clostridium group; Bacillales					26;		"Barbiturate-mediated regulation of expression of the cytochrome	P450BM-3 gene of Bacillus megaterium by Bm3R1 protein.";	992).			D97C2CFB57450EE8 CRC64;	Score 28; DB 2; Length 29; Pred. No. 8.1e-21; Mismatches 0; Indels	IDKPVQA 28	IDKPVQA 29		PRT; 730 AA.	Created) Last sequence update) Last annotation update)	
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	PRELIMINARY;	(TrEMBLrel.	(TrEMBLrel, 17,	(itemberet. i/, bas P450BM-3 (Fragment).	qaterium.	irmicutes; Baci	; Bacillus.	1404;		OM N.A.	MEDLINE=92184811; PubMed=1544926;	Fulco A.J.;	e-mediated regu	ne of Bacillus r	em. 267:5515-55	EMBL; S87512; AAK19020.1;		A; 3	2.7%; Similarity 100.0%; 8; Conservative (	TIKEMPOPKTFGELKNLPLLNTDKPVQA	TIKEMPQPKTFGELKNLPLLNTDKPVQA	}- }-	PRELIMINARY;	(TremBLrel. 20, (TremBLrel. 20, (TremBLrel. 21,	
RESULT 1 09AE23	Q9AE23 09AE23:	01-JUN-2001	01-JUN-2001	Cotochrome P450BM-3	Bacillus megaterium.	Bacteria; Firmicutes;	Bacillaceae; Bacillus.	NCBI_TaxID=1404;	[1]	SEQUENCE FROM N.A.	MEDLINE=921	Shaw G.C., Fulco A.J.;	"Barbiturat	P450BM-3 gel	J. Blol. Ch	EMBL; S8751;	NON TER	ы	Query Match Best Local Sim Matches 28;	1 TI	. 2 TII	RESULT 2	OBXIWO OBXIWO	01-MAR-2002 01-MAR-2002 01-MAR-2002	
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SERAIN-BRME-1767;
STRAIN-BRME-1767;
MEDLING-20136378; PubMed=10672447;
Yadav J.S., Loper J.C.;
"Cytochrome P450 oxidoreductase gene and its differentially terminated coDNAs from the white rot fungus Phanerochaete chrysosporium.";
EMBL; AF193062; AAG31351.1;
HSSP; P00388; LAMO.
InterPro; IPR001094; FAD_binding.
InterPro; IPR001226; Flavodoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phanerochaete chrysosporium.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Corticiaceae; Phanerochaete.
NCBI_TaxID=5306;
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Aphyllophorales; Corticiaceae; Phanerochaete.
NCBI_TaxID=5306;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNV-2002 (TrEMBLrel. 21, Last annotation update)
NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4).
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4)
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100.0%; Pred. No. 5.2e-05;
.ive 0; Mismatches 0; Indels
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InterPro; IRR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00158; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
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                                           899 IMVGPGTGVAPFRGF 913
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Matches 14; Conservative
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                                                                 Coriolus versicolor.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Aphyllophorales; Coriolus.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5061;
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van den Brink J., van Zeijl C., van den Hondel C., van Gorcom R.;
"Cloning and characterization of the NADPH cytochrome P450
oxidoreductase (cprA) gene of Aspergillus niger.";
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; 226938; CAA81550.1;
HSSP; P16435; IBC.
                                                                                                                                                                                                                                                                        Ichinose H., Wariishi H., Tanaka H.;
"Identification of cytochrome P450 oxidoreductase from white-rot
basidiomycete Coriolus versicolor.";
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                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AB063368; BAB83588.1;
InterPro: PPR003097; FAD_binding.

InterPro: IPR001205; Flavdoxin_like.

InterPro: IPR001226; Flavdoxin_like.

InterPro: IPR001226; Flavdoxin_like.

InterPro: IPR001043; FPN_CYL_redctse.

InterPro: IPR0010433; Oxred_FAD/NAD(P).

Pfam; PF00569; FAD_binding; 1.

Pfam; PF00758; flavodoxin; 1.

Pfam; PF00175; NaD_binding; 1.

Pfam; PF00175; NaD_binding; 1.

Pfam; PF00175; NaD_binding; 1.

PRINTS; PR00369; FLAVDDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6%; Score 17; DB 3; Length 730;
100.0%; Pred. No. 4.2e-08;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80742 MW; DB6FBC5FF3B15730 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    693 AA; 77072 MW; 1BEF35D4FC767674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
NADPH cytochrome P450 oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 693 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR003097; FAD_binding.
InterPro: IPR003097; FAD_binding.
InterPro: IPR001205; Flavdoxin.
InterPro: IPR001205; Flavdoxin.
InterPro: IPR001209; FPN_cyt_redctse.
InterPro: IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
PRIMTS; PR00369; FLAVDDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Cytochrome P450 oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  899 IMVGPGTGVAPFRGFVQ 915
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nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          730 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                      NCBI_TaxID=57466;
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Q00141 Q00141;

RESULT 3 Q00141

Matches

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Best Loca Matches

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Homo sapiens (Human).
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 Query Match
Best Local Similarity
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                                                                                                                                    Q9UHB4;
Q9UHB4;
01-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                        Matches
                                                                                                             RESULT 7
Q9UHB4
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Submitted (FEB-1999) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5 (BY SIMILARITY).
-!- CATALYJIC ACTIVITY: NADPH + 2 FERRICYTOCHROME - NADP(+) + 2
FERROCYTOCHROME.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00369; FLAVODOXÍN.
PRINTS; PR00371; FPNCR.
Hypothetical protein; Oxidoreductase; Flavoprotein; FMN; FAD; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FWN (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER
MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION (BY SIMILARITY).
-!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 NADP (RIBOSE PART) (BY SIMILARITY).
64199 MW; 12D64991612E7E00 CRC64;
                                                                                                                                                                                                                        ö
                                                                                                                                                                                              1.3%; Score 14; DB 3; Length 736; 100.0%; Pred. No. 5.5e-05; tive 0; Mismatches 0; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative NADPH-cytochrome P450 reductase (EC 1.6.2.4).
SPAC1296.06
                                                                                                                                                                        736 AA; 81627 MW; AC45F12C96198AB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast)
                                InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001206; Flavdoxin.
InterPro; IPR001709; FPN_Cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00265; FAD_binding; 1.
Pfam; PF00258; Flavdoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL035439; CAB36512.2; -.
HSSP; P00388; IAMO.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001256; Flavdoxin.
InterPro; IPR001709; PPN_Cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                       PRT;
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NP_BIND 524 542 NAC
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Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
AF193061; AAG31350.1; -. AF193060; AAG31349.1; -. P00388; 1AMO.
                                                                                                                                                                                                                                                902 GPGTGVAPFRGFVQ 915
                                                                                                                                                                                                                                                              14; Conservative
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Best Local Similarity
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                                                                                                                                                             Oxidoreductase
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                                                               Gaps
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MEDLINE-20092928; PubMed=10625700;
Paine M.J., Garner A.P., Powell D., Sibbald J., Sales M., Pratt N., Smith T., Tew D.G., Wolf C.R.;
Smith T., Tew D.G., Wolf C.R.;
Reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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1.2%; Score 13; DB 3; Length 558; 100.0%; Pred. No. 0.00046; Live 0; Mismatches 0; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015735; ARH15735.1; -.
INTERPRO; IPR003097; FAD_binding.
InterPro; IPR001226; Plavodoxin.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
NADPH-dependent FMN and FAD containing oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMB on PAD containing oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.2%; Score 13; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597 AA.
                                                                                                                                                                                                                                                                                                             597 AA.
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Interpro; IPR001433; Oxred_FAD/NAD(P)
Pfam; PF00067; FAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
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EMBL; AF199509; AAF25205.1; -.
HSSP; P00388; IAMO.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001265; Flavdoxin_like.
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PRINTS; PR00371; FPNCR.
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                                                                                                                                                899 IMVGPGTGVAPFR 911
                                                            13; Conservative
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InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
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Q9KF76;
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Q9P4E1;
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Q9P4E1
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          셤
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Rabourlaet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Brouillet S., Deviner K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,
RA Chia S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Rabitan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Raitan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Raitan K.D., Enrington J., Fabret C., Ferrari E., Foulger D.,
Raits C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
R. Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Antibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kutita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Hedina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Ronoe D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Reger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Roseto, M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tasconi E., Takagi T., Tarahashi H., Takemaru K.,
Roseto, W., Wedler E., Wedler E., Wedler H., Weitzenegger T.,
R. Winters P., Winder D., Wender E., Wedler H., Weitzenegger T.,
R. Wonnell M., Tanamokoshi A., Tanamoko H., Vamane K., Yasamoto K., Yata K.,
R. Yoshida K., Yoshikawa H., Dannen K., Yasamoto K., Yata K.,
R. Yoshida K., Yoshikawa H., Dannen K., Yasamoto K., Yata K.,
R. Wennell M., Wennell M., Wender E., Wendeler H., Wendeler M., We
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                                                                                                                                                                                                                                                                Gaps
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Sulfite reductase [NADPH] flavoprotein alpha-component-like protein
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Bacillaceae; Bacillus.
NCBL_TaxID-1423;
                                                                                                                                                                                              1.2%; Score 13; DB 4; Length 597;
100.0%; Pred. No. 0.00049;
ive 0; Mismatches 0; Indels
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299121; CAB15349.1; -.
HSSP: P00388; 1AMO.
                                                                                          Pfam; PF00175; NAD_binding; 1.
SEQUENCE 597 AA; 66776 MW; E1C340CF93A95534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 AA.
IPR001433; Oxred_FAD/NAD(P).
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InterPro; IPR001094; Flavdoxin_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
                              Pfam; PF00667; FAD_binding; 1
Pfam; PF00258; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                          11111111111
454 IMVGPGTGVAPFR 466
                                                                                                                                                                                                                                                                                                                         899 IMVGPGTGVAPFR 911
                                                                                                                                                                                                                     Local Similaricy
hes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis.
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   InterPro;
                                                                                                                                                                                                 Query Match
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032214
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                                                                                                                                                                                                                       Gaps
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EMBL; APO01509; BAB04328.1; -- HSSP; P00388; IAMO.
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MEDILINE-20512582; Pubmed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
NCBI_TaxID=86665;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4)
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                                                                                                                                                                     Length 605;
                                                                                                                                                                                                                     Indels
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                                                                                                                    605 AA; 67259 MW; 486F512COAED6217 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sulfite reductase (NADPH).
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                                                                                                                                                                  1.2%; Score 13; DB 16; L
.00.0%; Pred. No. 0.0005;
.ve 0; Mismatches 0;
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Interpro; IPR001226; Flavdoxin.
Interpro; IPR001709; FPN_cyt_redctse.
Interpro: IPR00143; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
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Pfam; PF00667; FAD_binding; 1.
                      Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
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                                                                                                                                                                                           100.08;
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PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                   899 IMVGPGTGVAPFR 911
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Matches 13; Conservative
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans.
                                                                                             Complete proteome. SEQUENCE 605 AA;
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Pred. No. 0.00055;
                                                                                                                                                                                                                                                                                                                       710 AA.
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR0011226; Flavdoxin.
InterPro; IPR001199; FPN_cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00559; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel, 15, Created)
01-0CT-2000 (TrEMBLrel, 15, Last seq
01-JUN-2002 (TrEMBLrel, 21, Last ann
                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=20564350; PubMed=10995755;
100.08; Pro
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PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                               902 GPGTGVAPFRGFV 914
                                                                                                                                             902 GPGTGVAPFRGFV 914
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nes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cunninghamella elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4853;
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                                                                                                                                                                                                                                                             RESULT 13
Q9P4E2
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                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 26878;
MEDLINE-20145435; PubMed-10679206;
Xadav J.S., Loper J.C.;
"Cloning and characterization of the cytochrome P450 oxidoreductase gene from the zygomycete fungus Cunninghamella.";
Biochem. Biophys. Res. Commun. 268:345-353(2000).
HSSP; P16435; 1B1C.
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Function cloning based on azole resistance in S. cerevisiae and
characterization of R. nigricans redox carriers differentially
involved in P450 dependent response to progesterone stress.";
EMBL; AF290425; AAG23833.1;
HSSP; P00388; IAMO.
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01-MAR-2002 (TremBirel. 20, Last annotation update)
NADPH cytochrome P450 oxidoreductase isoenzyme 1 (EC 1.6.2.4).
Rhizopus stolonifer (Rhizopus nigricans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 13; DB 3; Length 629;
100.0%; Pred. No. 0.00052;
.ive 0; Mismatches 0; Indels
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                                                                                Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
Cunninghamellaceae; Cunninghamella.
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR0010226; Flavdoxin.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
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InterPro: IPR001094; Flavdoxin_like.
InterPro: IPR001205; Flavdoxin.
InterPro: IPR001709; FPN_CYt_redctse.
InterPro: IPR001433; Oxred_FAD/NAD(P)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF00667; FAD_binding; 1.
Pfam: PF00258; flavodoxin; 1.
Pfam: PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
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Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
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PRINTS; PR00371; FPNCR.
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                                                 Cunninghamella echinulata
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les 13; Conserv
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                                                                                                                                    NCBI_TaxID=76405;
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SEQUENCE
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**09HFV3** 

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(EC 1.14.14.1);
  Gaps
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"Fusarium oxysporum fatty-acid subterminal hydroxylase (CYP505) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20145435; PubMed=10679206; Yadav J.S., Loper J.C.; 
Yadav J.S., Loper J.C.; 
"Cloning and characterization of the cytochrome P450 oxidoreductase gene from the zygomycete fungus Cunninghamella."; 
Blochem. Blophys. Res. Commun. 268:345-353(2000). 
EMBL; AF195659; AAF89958.1; -. 
HSSP; P16435; 1B1C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
NCBL_TaxID=5507;
                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.2%; Score 13; DB 3; Length 710;
100.0%; Pred. No. 0.00058;
ive 0; Mismatches 0; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Bifunctional P-450:NADPH-P450 reductase protein (Fatty hydroxylase) (P450foxy) [Includes: cytochrome P450 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        710 AA; 80021 MW; 8B3443AF5CDA3565 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Żygomycota; Zygomycetes; Mucorales;
Cunninghamellaceae; Cunninghamella.
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STRAIN=A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
              SEQUENCE FROM N.A.
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                                                                                           Nakayama N., Takemae A., Shoun H.;
"Cytochrome P450foxy, a catalytically self-sufficient fatty acid
hydroxylase of the fungus Fusarium oxysporum.";
-1. Blochem. 119:435-440(1996).
-1. FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. SHOWS HIGHEST
ACTIVITY TOWARD FATTY ACIDS WITH A CHAIN LENGTH OF 12-14 CARBONS.
THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                 -!- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FWN (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PROUGLE; rejou.
PROSITE; PROUGLE; CYTOCHROME_P450; 1.
Heme; Monooxygenase; Oxidoreductase; Membrane; Electron transport;
Houltifunctional enzyme; FMN; FAD; Flavoprotein; NADP.
DOMAIN 1 480 CYTOCHROME P450.
DOMAIN 481 1066 NADPH-P-450 REDUCTASE.
BINDING 407 407 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                  TO CYTOCHROME P450.

-I CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)0.

-I - CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
membrane-bound eukaryotic counterpart of Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2%; Score 13; DB 3; Length 1066; 100.0%; Pred. No. 0.00085; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A3(2);
Saunders D.C., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative cytochrome P450.
SC00801 OR SCF43.12.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          527 AA.
                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001128; Cytochrome_P450.
Interpro; IPR001309; FAD_binding.
Interpro; IPR001304; FAD_binding.
Interpro; IPR001205; Flavdoxin.
Interpro; IPR001205; Flavdoxin.
Interpro; IPR001433; Oxred_FAD/NAD(P).
Ffam; PF00667; FAD_binding; I.
Pfam; PF00258; flavodoxin; I.
                          Biol. Chem. 275:39734-39740(2000).
                                                      FUNCTION, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                  STRAIN-MT-811;
MEDLINE-96271003; Pubmed-8830036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
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PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 ITFLIAGHETTSG 273
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Best Local Similarity
             cytochrome P450BM3
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                                                                       Redenbach M., Kleser H.M., Denapatte D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
*A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicalor A3(2) chromosome.";
*Mod. Microbiol. 21:77-96(1996).
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares R., Ruther S.,
Wartens T., Wletzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of the model actinomycete Streptomyces
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PROSITE; PS00277; TUBULIN; 1.
Heme: Monooxygenase; Oxidoxeductase.
SEQUENCE 527 AA; 57741 MW; 4A612C1B7A894780 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; ALJ35502; CAB66201.1; -.
HSSP; P14779; 1BVY.
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.00.0%; Pred. No. 0.0048;
.ve 0; Mismatches 0;
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InterPro; IPR000217; Tubulin.
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Job time : 100 secs
                          STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
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Matches 12; Conservative
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PRINTS; PR00385; P450.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 29, 2003, 08:22:16; Search time 74 Seconds Run on:

(without alignments)
1887.117 Million cell updates/sec

US-10-031-146-2 5457 1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA19 A\_Geneseq\_101002:\*

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988. /SIDSŽ/gcgdata/geneseg/genesegp-emb1/AA1980 /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1981. /SIDS2/gcgdata/geneseg/genesegp-embl/AA1983/SIDS2/gcgdata/geneseg/genesegp-embl/AA1984

cgdata/geneseq/geneseqp-emb1/AA1989.

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992 /gcgdata/geneseq/geneseqp-embl/AA1994 /SIDS2/gcgdata/geneseq/genesegp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query	Query Match Length DB ID	98	ΙD	Description .
7	5457	100.0	1048	52	AAB31978	Amino acid sequenc
7	5457	100.0	1048	22	AAB46855	B. megaterium cyto
m	5457	100.0	1048	22	AAB46856	B. megaterium cvto
4	5457	100.0	1049	21	AAY93566	Amino acid sequenc
Ŋ	5457	100.0	1049	22	AAB31882	Amino acid sequenc
9	5450	6.66	1048	22	AAB31979	Amino acid sequenc
7	5449	99.9	1049	22	AAY72208	Bacillus megateriu
œ	5444	99.8	1048	22	AAB31980	Amino acid sequenc
6	5440	99.7	1048	22	AAB31981	Amino acid sequenc
10	3154.5	57.8	1085	12	AAR11604	P450 17-alpha/P450

Expression prod. o Mouse lischaemic co	Plasmid pRF1 rat 1 NADPH cytcohrome P Sequence of rabbit Rabbit NADH cytoch Human full-length Human contig colyo		anchor P450 r sion pr phila n hondric cytoch	Plant NADPH Cytoch Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Helianthus tuberos Helianthus tuberos Poppy cytochrome P
AAP81334 AAP81337 AAP81335 AAP81336 AAP81338			∢	14 AAR43581 21 AAG35842 21 AAG35840 22 AAG35840 23 AAE20656 23 AAE16392 20 AAW85681 14 AAR43582 14 AAR44589
1144 9 1150 9 1150 9 1162 9 1132 9 678 2				692 1 697 2 701 2 711 2 588 2 704 2 712 1 1429 1
17.8 17.7 17.6 16.8 16.6	224400	0001111	.v.v.w.w.v.o.o	133.0 123.0 122.0 122.9 122.9
971.5 968.5 962.5 916.5 906.5	774.5 772.5 769 769 766	761 761 747 747 747	737.5 737.5 726 725.5 723.5 711.5	710.5 709 709 709 705.5 703.5 703.5 695.5 678
11 12 14 15	17 19 20 21 21	2 2 2 2 2 3 2 3 3 4 3 5 4 3 5 4 3 5 4 3 5 4 3 5 4 3 5 4 3 5 4 3 5 5 5 5	33333333333333333333333333333333333333	. 0 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

### ALIGNMENTS

Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin. Amino acid sequence of a Bacillus P450 monooxygenase protein. AAB31978 standard; Protein; 1048 AA 27-JUL-1999; 99DE-1035115. 18-NOV-1999; 99DE-1055605. 22-MAR-2000; 2000DE-1014085. 27-JUL-2000; 2000WO-EP07253. 15-MAY-2001 (first entry) Bacillus megaterium. WO200107630-A1. 01-FEB-2001 AAB31978; **AAB3197**8 

Hauer B, Pleiss J, Li Q; (BADI ) BASF AG.

Fischer M, Schmitt J, Schwaneberg U,

WPI; 2001-182800/18. N-PSDB; AAF54832.

Cytochrome P450 monooxygenase for oxidizing organic compounds, useful

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                                                                                                                                                                                                                                                                                                                                   ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMY 120
                                                                                                                                                                                                                                                                                                                                                                       DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA 180
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                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono- or poly-cyclic aromatic heterocyclics containing nitrogen, sulphur or oxygen; optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkenes. The modified cytochrome P450 monooxygenase are specifically used to oxidize indole to indigo and indorublicin. However, they may be used to oxidize many
                                                                                                                                                                                                                                                                                 1 TIKEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSGRLIKE
                                                                                                                                                                                                                                                                   1 TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG
especially for converting indole to indigo, has wide substrate range
                                                                                                                                                                                                                                           0; · Gaps
                                                                                                                                                                                                                    Length 1048;
                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                           Mismatches
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                       Claim 3; Page 35-39; 54pp; German.
                                                                                                                                                                                          1048 AA;
                                                                                                                                                                  other substrates.
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This invention describes a novel electron donor system (M1) that
transfers electrons to an enzyme with redox properties comprising an
inorganic, not electrode-bound, electron sink and a mediator which enable
the electron transfer. The invention also describes (1) transferring (M2)
oxygen to a hydrocarbon containing hydrogen donor molecule, where the
hydrogen donor molecule is in a reaction medium comprising the oxygen
transferring enzyme and (M1) in the presence of oxygen and incubating
under suitable reaction conditions; (2) the enzymatic production (M3) of
terminally or subterminally hydroxylated (position omega-1 to omega-4)
certificative in the presence of (M1) and cytochrome P450
monooxygenase; and (i1) isolating the hydroxylated product; (3) a
cold derivative in the presence of (M1) and cytochrome P450
monooxygenase; and (i1) isolating the hydroxylated fatty acids as described in (2); and (4) detecting (M4) fatty acid-monooxygenases
comprising: (1) contacting the analyte with a omega-hydroxylatable fatty
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                                                                                                                      Novel electron donor system useful for the production of omega-hydroxylated fatty acids comprises an inorganic electron sink and a mediator which enables the electron transfer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bioreactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor; electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase.
                                    QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM
     EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK
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10-MAR-2000; 2000DE-1011723.
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        label in (M1); and (ii) qualitatively or quantitatively detecting the signal. The invention is useful for the production of omega-hydroxylated fatty acids and the detection of fatty acid monooxygenases. The invention provides an alternative electron donor system of enzymes with redox properties that is cheaper and more efficient, where the enzyme
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 terminal chromophore or
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                  VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
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                                                                                                                                                                                                                                                                                                                                             B. megaterium cytochrome P450 monooxygenase BM-3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Process for oxidizing acyclic or cyclic terpenes, cycloalkenes, or derivatives for preventing or treating infection in human or animal body comprises mutant haem-containing enzyme which has substitution of amino acid in the active site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a process for oxidizing an acyclic or cyclic terpene, a cycloalkene, or a derivative. The process comprises oxidizing the compound with a mutant haem-containing enzyme which comprises a substitution of an amino acid in the active site by an amino acid with a less polar side-chain. The process is useful for oxidizing an acyclic or cyclic terpene, a cycloalkene, or their derivatives. The process is also useful for product useful for preventing or treating infection in a human or animal body. The present sequence represents the amino acid sequence of the p450-BM3 sequence. The protein is used to construct enzymes for use in the process of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TIKEMPOPKTFGELKNLPLLNTDKPVOALMKIADELGEIFKFEAPGRVTRYLSSORLIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
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                                              cycloalkene; haem-containing enzyme; mutant; oxidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1049;
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  P450-BM3 sequence
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Misc-dlfference 303
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  Amino acid sequence
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                                                                           infection; P450-BM3
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                                                                                                                             Unidentified
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monooxygenase; oxidization; indole; indigo; indorubicin
                                                                                                                                                                                                                                                              The present sequence represents a cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono- or poly-cyclic aromatic heterocyclics containing nitrogen, sulphur or oxygen, optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkenes. The modified cytochrome P450 monooxygenase are specifically used to oxidize indole to indigo and indorubicin. However, they may be used to oxidize many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                     LDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG
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                                                                                                                                                                                                              organic compounds, useful has wide substrate range
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                                                                                                                                                                                                              P450 monooxygenase for oxidizing for converting indole to indigo,
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                                                                                                                                                                                                                                            Disclosure; Page 41-44; 54pp; German.
                                                                                                                                                              Schwaneberg U,
                                                                                                                                                                                                            Cytochrome P450 monooxygenase for especially for converting indole t
                                                                                                  27-JUL-1999; 99DE-1035115.
18-NOV-1999; 99DE-1055605.
22-MAR-2000; 2000DE-1014085.
                                                                               27-JUL-2000; 2000WO-EP07253
                                                                                                                                                              Pleiss J,
                                                                                                                                                                                           WPI; 2001-182800/18
                      Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                              1049 AA;
                                                                                                                                                                                                                                                                                                                                                          other substrates
 Cytochrome P450
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            HTAFSRMPNQPKTYVQHVWEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV
                                              AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
                                                                                                                                                     QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM
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FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT
                                       PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR
                                                                 GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG
                                                                                                                     DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL
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                                                                                                                                                                                                The present sequence represents a modified cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono- or poly-cyclic aromatic heterocyclics containing nitrogen, sulphur or oxygen; optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkanes or alkenes; or optionally substituted cycloalkanes or cycloalkanes are specifically used to oxidize indole to indigo and indorubicin. However, they may be used to oxidise many
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                                                                                                                                                                                                                                                                                                                                                                                        this sequence does not appear in the specification; it was created information provided.
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  Schwaneberg
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compounds. Also mutants of the monooxygenase enzyme with substitutions in the active site have enhanced oxidation activity. The process and the transgenic plant or animal which expresses the monooxygenase enzyme are used for detoxifying the environment polluted with the halo aromatic compounds. The present sequence is a Bacilius megaterium monooxygenase enzyme, P450BM-3, which is homologous to the monooxygenase
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            QASITVSVVSGEAWSGYGEYKGIASNYIAELQEGDTITCFISTPQSEFTLPKDPETPLIM
                                                                                                                                                             VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
                                                                                                                                                                                                          AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
                                                DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL
                                                                                                EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monooxygenase enzyme; P450BM-3 homologue; P450cam; oxidation; halogenated aromatic compound; electron transfer; putidaredoxin; putidaredoxin reductase; detoxification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    process for detoxifying environments contaminated with halo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aromatic compounds comprises treating the affected area with a monooxygenase enzyme -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus megaterium monooxygenase enzyme homologue, P450BM-3.
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                                                                                                                                                                                                                                                                                                             Disclosure; Page 32-39; 42pp; English.
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N-PSDB; AAD02365.
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                                 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD
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Best Local Similarity 99.7%;
Matches 1045; Conservative (
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18-NOV-1999; 99DE-1055605.
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Li Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-182800/18.
                                                                                                                                                                              Bacillus megaterium
                                                                                                                                                                                                                                                                        Misc-difference 188
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                                                                                                                                                                                                                                              Misc-difference 87
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                                                                                                                                                                                                                                                                                                             WO200107630-A1
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18-NOV-1999;
                                                                                                  15-MAY-2001
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                                                                        AAB31981;
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 470 DGKLPSLEGHASLVLQIKPFKVKIEVRQ-----AWKEAQAEGSTPGTAENAHNTPLLV
                         NVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQ
                                                                                                                                                                                     QIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALL
                                                                         KQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEAD
                                                                                                                                                                                                                                   TGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAF
                                                                                                                        ASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHGAFST
                                                                                                                                                                                                                                                                    EKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASI
                                                                                                                                                                                                                                                                                                                    TVSVVSGEAWSGYGEYKGIASNYLAELOEGDTITCFISTPOSEFTLPKDPETPLIMVGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oxidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADPH cytochrome p-450; reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1025 EADARLWLQQLEEKGRYAKDVWAG 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1063 EADARLWL-QLEEKGRYAKDVWAG 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression prod. of plasmid pAMP19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; ; p; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome p450; industrial waste.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIIT --- FLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVL - VDPVPSYKQVKQLK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVGMVLNEALRLWPTAPAFSLY-AKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWGDDV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                                                                        The protein is a fusion of bovine adrenal cytochrome P450 17-alpha and Bacillus megaterium-derived cytochrome P450 BM-3. The fusion protein has the monoatomic oxygenation activity of the former and the reductivity supplying activity of the latter. Plasmid p(alphaBM1), containing the recombinant sequence encoding the fusion protein, is used to transform Saccharomyces cerevisiae. The transformant is designated AH22(p(alphaBM-1)) and can be used for the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- DGLFTSWTHEKNWKKAHNILLPSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------EDPALKAIQNVN--DGILEVLSKEVLLDIFPVLKIFPSKAMEKMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQAMKGYHAMMVDIAVQLVQKWERLNADEH---IEVPEDMTRLTLDTIGLCGFNYRFNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KVMNDLVDKIIADRKASGEQSDDLLTHMLN-----GKDPETGEPLDDENI---RY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEFRPERFENPSAI----PQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKHFDFE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRDQPHPFITSMVRALDEAMNKLQRANPDDPAYDENKRQFQEDI--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                   P450 reductase fused oxidase coding gene - has both mono-atomic oxygenation activity of bovine adrenal cytochrome p450 17-alpha and reductivity supplying activity
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 1085;
                        bovine adrenal; cytochrome P450; oxidase; reductase; steroid;
plasmid p(alphaBM1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          57.8%; Score 3154.5; DB 12
60.9%; Pred. No. 1.2e-211;
.1ve 105; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESRFDKNLSQALKFVRDFAG------
P450 17-alpha/P450 BM-3 fusion protein.
                                                                                                                                                                                                                                                                    8pp; Japanese,
                                                                                                                                  89JP-0197296
                                                                                                                                                           (SUMO ) SUMITOMO CHEM IND
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N-PSDB; AAQ11474.
                                                                                                                                                                                                                                                                                                                                                                                                      1085 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
672; Conser
                                                                                                                                                                                                                                                                    Claim 1; Fig 2;
                                                           JP03061490-A.
                                                                                                            28-JUL-1989;
                                                                                                                                  28-JUL-1989;
                                                                                   18-MAR-1991
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××			Qy 879 CFISTPOSEFTL
ខ្ល	See also AAN81744-48.		477
SO	Sequence 1144 AA;		
Õää	Query Match 17.8%; Score 971.5; Best Local Similarity 28.3%; Pred. No. 7.4e Matches 320; Conservative 186; Mismatches	); DB 9; Length 1144; .4e-59; Les 468; Indels 157; Gaps 43;	OY 939 FREDILL CEELLE 
ογ	ALMKIADELGEIFKFEAPGRVTRYLSSC	80	Oy 997 YICGDGSQMAPA
QQ ,	63 PHLSLTKLSQYGDVLQIRIGSTPVVVLSGLNTIKQA	KQALVKQGDDFKGR 110	
ογ	85 GLFTSWTHEKNWKKAHNILLPSFSQQAMKGY	SFSQQAMKGYHA 117	RESULT 12
QQ	111 PDLYSFTLIANGQSMTFNPDSGPLWAARRRLAQNALKSFSIASDPTLASSCYLEE	:   :  ; AQNALKSFSIASDPTLASSCYLEE 165	AAP8133/ ID AAP81337 standard; pro
δλ	118 MMVDIAVQLVQKWERLNAD-EHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITS	DIIGLCGFNYRFNSFYRDQPHPFITS 176	AA AAP81337;
q	166 HVSKEAEYLISKFOKLMAEVGHFDPFKYLVVSVANVICAICFGRRXDHDDQELLSIVN		DT 19-OCT-1990 (first el
δλ	177 MVRALDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKA	ENKRQFQEDIKVMNDLVDKIIADRKA 225	DE Expression prod. of p
q	224 LSNEFGEVTGSGYPADFIPILRYLPNSSLDAFKDLNKKFYSFWKKLIKEHYR	LIKKFYSFMKKLIKEHYR 275	KW Cytochrome p450; NADP
ço q	226 SGEQSDDLLTHMLNGK-DPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALY		XX PN JP63044888-A.
3 8			XX PD 25-FEB-1988.
2 2	2/9 FLVKRPHVLOKAAEEAARVL-VDPVPSYKQVKQVKQUKYVGMYLNEARRIMPTAPAFSLYA  -	KYVGMVLNEALRLWPTAPAFSLYA 335 	XX PF 12-AUG-1986; 86JP-0
à	TATION TATION TO THE TAXABLE PROPERTY OF T		PR 12-AUG-1986; 86JP-0
2 8	395 IRDJSGLNGY-IPKGHCYVVNONOVNHODELWGDP-NEREKERKENFS-ALQHARRY 395 IRDJSGLNGY-IPKGHCYVVNONOVNHODELWGDP-NEREKETASGTILDRHISEKVI		XX PA (AGEN ) AGENCY OF IND XX
à			DR WPI; 1988-094816/14.
ф		:: : SPGEKVDMTPAYGLTLKHARCEHFQV 512	
Οy	447 KAKSKKIPLGGIPSPSTEQS-AKKVRKAENAHNTPLLVLYGSNMGTAEGTARDLADI	HNTPLLVLYGSNMGTAEGTARDLADI 503	
QQ	513 QMRSSGPRAMIQTTAPPVKESSFVEKWKKTGRNIIVFYGSQTGTAEEFANRLSKD	IIVFYGSQTGTAEEFANRLSKD 567	
δλ	504 AMSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQFVDMLDQASA	VTASY-NGHPPDNAKQFVDWLDQASA 556	XX XX Common 1150 AX.
qq	568 AHRYGMRGMSADPEEYDLADLSSLPEIDKSLVVFCMATYGEGDPTDNAQDFYDWLQETDV	CMATYGEGDPTDNAQDFYDWLQETDV 627	anientec
oy S	557 DEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENTADRGEADASDDFEGTY		Whely malch Best Local Similarity Matches 320; Conservat
g ;	628 D-LTGVKFAVFGLGNKTYEHFNAMGKYVDC		Qy 25 PVQALMKIADEL
<u> </u>	014 EEWKEHMWSDVAAIFNIDIENEDNKSTESLQEVUSAADMPLAKHH	USAAUMPLAKMH	:   :: :   DD 63 PHLSLTKLSQQY
ò			Qy 85 GLFTSWTHEKN-
. d			Db 111 PDLYSFTLIANG
δŏ	713 RVTARFG LDASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAK		Qy 118 MWVDIAVQLVQK
qq	::       :		Db 166 HVSKEAEYLISK
δy	771 TVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSI	TMLELLEKYPACEMKFSEFIALLPSI 824	
QQ	858 YASEPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDYPSLRPPIDHLCELLPRL	:  : :   : HILAILQDYPSLRPPIDHLCELLPRL 917	224
δλ	825 RPRYXSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDTIT	EYKGIASNYL-AELQEGDTIT 878	QY ZZ6 SGEQSD :   :   :   :   :   :   :   :   :   :
අු	918 QARYYSIASSSKVHPNSVHICAVAVEYEAKSGRVN-KGVATSWLRAKEPAGENGGRALVP	N-KGVATSWLRAKEPAGENGGRALVP 976	279

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43;
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| GQSMTFNPDSGPLWAARRL----AQNALKSFSIASDPTLASSCYLEE 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYPADFIPILRYLPNSSLDAFKDLNKKFY-----SFMKKLIKEHYR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDLLTHMLNGK-DPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALY 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 FLVKNPHVLQKAAEEAARVL-VDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSL--YA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        le gene - coding oxidation enzyme of cytochrome p-450
! p-450 reduction enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGEIFKFEAPGRVTRYLSSQRLIKEACDESRFDKNLSQALKFVRDFAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 163; Gaps
                                                                                                                                AVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                                                                                                                                                                                                                                      PH cytochrome p-450; reduction; oxidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.7%; Score 968.5; DB 9; Length 1150; 28.1%; Pred. No. 1.2e-58; tive 186; Mismatches 468; Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and AAN81747-48.
                                                                                                                                                                                                                                                   rotein; 1150 AA
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43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 FLVKNPHVLQKAAEEAARVL-VDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSL--YA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     629
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                                                                        Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450 and NADPH-cytochrome p-450 reduction enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|| || : :| || |: || || || || || || || 336 YLVTNPRIQRKIQEELDTVIGRDRQPRLSDRPQLPYLEAFILETFRHSSFVP-FTIPHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393 -FGNGQRACIGQOFALHEATLVLGMMLKHFDFEDHTNYELDIKET--LTLKP---EGFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 SGEQ-----SDDLLTHMLNGK-DPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 LFGLGKRKCIGETIGRLEVFLFLAILLQOMEFNVSPGEKVDMTPAYGLTLKHARCEHFQV
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                                                                                                                                                                                                                                                                                                                                                        163;
                                                                                                                                                                                                                                                                                                      Length 1150;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                    Match 17.6%; Score 962.5; DB 9; Local Similarity 28.1%; Pred. No. 3.2e-58; es 319; Conservative 186; Mismatches 469;
                                                                                                                                                                                                       See also AAN81743 and AAN81745-48
                                                                                                                                                        Disclosure; ; p; Japanese.
WPI; 1988-094816/14.
                                                                                                                                                                                                                                                        Sequence 1150 AA;
                            N-PSDB; AAN81744
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118 MAYDIAVQLYQKWERLNAD-EHIEVPEDMIRLTLDTIGLCGFNYRFNSFYRDQPHPFITS 176 :	279 FLVKNPIIVLQKAAEEAARVL-VDPVPSYKQVKQLKYVGMVLNEALRLMPTAPAFSLYA 335	393 -FGNGQRACIGQQFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVV 446	PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTA	TYGEGDPTDNAQDFYDWLQETDVD-LFGVKFAVFGLGNKTYEHFNAMGKIVDQRLE  AKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLGFVDSA	651 ADMPLAKHHEIEL-P 689  [	ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTML     :: ::       :       :           :	AILODYPSLRPPIDHLCELLPRLQARYYSIASSSKVHPNSVHICAVAVEYEAKSGRVN-K GIASNYL-AELOEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVO [:1:::    :	916 ARKOLKEDGOSLGEAHLYFGCRSPHEDYLYØEELENAOSEGIIT-LHTAFSRMPNQPKTY 974
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707 YEGIVNRVTAREGLDASQOIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQL :	•	1035 992 1094	AAPB1336 ID AAP81336 standard; protein; 1162 AA. XX AAP81336; XX DT 19-OCT-1990 (first entry)	DE EXPLESSION PLOG. OI PLASMIG PALPLY. XX KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation; KW industrial waste. XX PN JP63044888-A.	AX	A (AGEN ) AGENCY OF IND SCI TECH.  XX XX NPI; 1988-094816/14.  DR N-PSDB; AAN81745.  XX PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450 PT and NADPH-cytochrome p-450 reduction enzyme	XX PS Disclosure; ; p; Japanese. XX CC See also AAN81743-84 and AAN81746-48. XX SQ Sequence 1162 AA;	Query Match         16.8%;         Score 916.5;         DB 9;         Length 1162;           Best Local Similarity         27.2%;         Pred. No. 5.3e-55;         Ads-55;         Ads-55;           Matches 314;         Conservative 185;         Mismatches 469;         Indels 187;         Gaps 43;           QY         25 PVQALMKIADELGEIFKFEAPGRVTRXLSSQRLIKEACDESRFDKNLSQALKFVRDFAGD 84

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 PDLYSFTLIANGOSMTFNPDSGPLWAARRRL----AQNALKSFSIASDPTLASSCYLEE 165
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                                                                                                                                                                                                                                             p450; NADPH cytochrome p-450; reduction; waste.
                                              AAP81338 standard; protein; 1132 AA
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N-PSDB; AAN81747.
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498 AAADRAAADRAMIQTTAPPVKESSFVEKMKKTGRN----IIVFYGSQTGTAEEFANRL
                                                                                                                                             ADIAMSKGFAPQVATLDSH----AGNLPR--EGAVLIVTASY-NGHPPDNAKQFVDWLDQ
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earch completed: May 29, 2003, 08:28:33

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1713.068 Million cell updates/sec
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1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                      Scoring table:
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Maximum DB seq
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Appl Appli Appli Appli Appli Appli Appl Appli Appli Appli Appl Seguence 14, Appl Seguence 2, Appli Appli Appli Appli Appli Appli Description Sednence Sed Sequence Sequence 05-08-365-486A-13 05-08-319-866-11 05-08-800-342-13 05-08-705-625-4 05-09-10-998-5 05-09-220-574-4 05-09-123-708-4 05-09-123-708-4 05-09-123-708-4 05-08-365-486A-19 05-08-365-486A-19 05-08-365-486A-19 05-08-365-486A-19 05-08-365-486A-19 05-08-365-486A-19 05-08-365-486A-19 05-08-365-486A-19 US-08-147-812-5 US-08-319-866-12 US-08-465-522-2 PCT-US93-11401-2 -09-220-574-3 SUMMARIES Query Match Length DB Score М М Result

656 AKMHGA---FSTNVVASKELQQPGSARSTRHLEIELPKEA-SYQEGDHLGVIPRNYEGIV 711

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11 | : | : | : | 340 EEAEKLIGLPADTYFSLHIDNEDGTPLGGPTLQPPFPPCTLRKALTNYADLLSSPKKSTL 299 765 RAMAAKTVCPPHKVELEALLE---KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-AL 820

Sequence

712 NRVTARFGLDASQQIRLEAEEEKLAHL-----PLAKTVSVEELLQYVELQDPVTRTQL 764

Appli Appli			_	557	612	655 179
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00000000000000000000000000000000000000		Application 36887 RMATION: Satisslant, Satisslant, Tang, Xiao Ol, Wel We. Wornelli, Gatenby, An VENTION UNITED BLINCE: BCI009 LINCENBEL BLINCE: BCI009 LINCENBEL BLINCE: BCI009 LINCENBEL BLINCE: BCI000 LINCENBEL B	Conse	OIAMS	SV II SVWLE	VREHM  : : VKELV
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SRMPNQPKTYVQHVMEQDGKKLI--ELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQ 1022
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                                 --VDWLDQ-ASADEVKGVRYSVFGCGDKNWATTYQKVP 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         788 AYKEQVLAKRLIMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASITVS
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                                                                                                838 RKSYKVRFNSVSSYSDSRKSSGDGPDLRDNFESTGPLANVRFSVFGLGSR----AYPHFC
                                                                                                                                                           AF---IDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNL--DIENSED
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APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN DATE:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION UNDBER: 38,615
REFERENCE/POOCKET
TELECOMMUNICATION: INFORMATION:
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ZIP: 94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bredt, David S.
APPLICANT: Hang, Paul M.
APPLICANT: Hang, Paul M.
APPLICANT: Reed, Randall
APPLICANT: Snyder, Solomon H.
TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQF-----
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,002
FILING DATE: 19910118
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Patent No. 5268465
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- ATTORNEY/AGENT INRORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REPERENCE/DOCKEY NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 296-5500
INFORMATION FOR SEQ. 1296-5500
INFORMATION FOR SEQ. 10 NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 193; Conserv
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                      Query Match
12.4%; Score 678; DB 2; Length 1429;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches. 193; Conservative 126; Mismatches 265; Indels 100;
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APPLICANT: Yin, Jerry C.
APPLICANT: Regulski, Michael
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSEADARLWLQQLEEKGRYAKDVW 1046
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LSEEDAGVFISRLRDDNRYHEDIF 1395
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TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 amino acids
                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-365-486A-13
                                                                                     amino acid
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                    E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
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                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,866
FILING DATE: 7-OCT-1994
CLASSIPRCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: CSHL94-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
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CORRESPONDENCE ADDRESS:
                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                   Lexington
                                                                                                                     USA
                                                                                                                                       02173
                    ADDRESSEE:
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                                                                                                                   COUNTRY:
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APPLICANT: Jaffrey, Samie R.
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
TITLE OF INVENTION: Oxide Synthase
                       505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQF
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1372 LSEEDAGVFISRLRDDNRYHEDIF 1395
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30-AUG-1996
N: 530
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Patent No. 5908756
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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NAME: Kagan, Sarah A.
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CORRESPONDENCE ADDRESS:
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APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
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2.6e-50;
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350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 8255-0018.30 IELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                            1023 VSEADARLWLQQLEEKGRYAKDVW 1046
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LSEEDAGVFISRLRDDNRYHEDIF 1395
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APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
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28.2%;
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TELEFAX: (415) 324-0860
INPORMATION FOR SEG ID NO: 13.
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESSE: Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306
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SRMPNQPKTYVQHVMEQDGKKLI--ELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQ 1022
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778 KHAFDAKAMSMEEYDIVHLEHEALVLVVTSTFGNGDPPENGEKFGCALMEMRHPNSVQEE 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 12.4%; Score 678; DB 2; Length 1430;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQF------
                01107.57071
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1372 LSEEDAGVFISRLRDDNRYHEDIF 1395
              REFERENCE/DOCKET NUMBER: 0110
TELECOMMUTCATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISICS:
LENGTH: 1430 amino acids
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                           amino acid
                                                                                                                                                                                                              ORIGINAL SOURCE:
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Sequence 5, Application US/09010998 Patent No. 6103872

US-09-010-998-5

RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457 GIPSPSTEQSAKKVRKKAE------NAHNTPLLVLYGSNMGTAEGTARDLADIA
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                                APPLICANT: Snowman, Adele
APPLICANT: Eliasson, Mikael
APPLICANT: Cohen, No. 6103872m
TITLE OF INVENTION: CAPON, a protein that binds
TITLE OF INVENTION: neuronal nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01107.73424
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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US-09-010-998-5
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                                                                                                                                                                                                                                                                                                       E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
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Snyder, Solomon
                  Jaffrey, Samle
Snowman, Adele
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                           STATE: DC
COUNTRY: US
ZIP: 20001
                                                                                                                                                                                                                                                                                                                         COMPUTER:
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965 SRMPNQPKTYVQHVMEQDGKKLI--ELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQ 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NAHNTPLLVLYGSNMGTAEGTARDLADIA 504
                                                                                                                                GINGTPIKRRAIGFKKLAEAVKFSAKLMGQAMAKRVKAIILYAIEIGKSQAYAKTLCEIF 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 638 NKSTLS------LQFVDSAADMP--LAKMH--GAFSTNVVASKELQQPGSARSTR 682
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                                                                                                                                                                                                                                      | :: : :| | ||:||::|| ||:|| 1378 KHAFDAKAMSMEEYDIVHLEHEALVLVVTSTFGNGDPPENGEKFGCALMEMRHPNSVQEE
                                                                                                                                                                                                                                                                                                                                                                                               838 RKSYKVRFNSVSSYSDSRKSSGDGPDLRDNFESTGPLANVRFSVFGLGSR----AYPHFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739 PLAKTVSVEELL-----QYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE-KQ
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                                                                                                                                                                                                                                                                                                                                  ---VDWLDQ-ASADEVKGVRYSVFGCGDKNWATTYQKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     907 VAPFRGFVQARK-QLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGII-TLHTAF
      Indels 100; Gaps
                                                                                                                                                                                                 505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQF----
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APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
      Mismatches 265;
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   Conservative 126;
                                                                       GIPSPSTEQSAKKVRKKAE---
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COUNTRY: · USA
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US-08-365-486A-21
      Matches 193;
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                                                                                                                                                                  788 AYKEQVLAKRLIMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASITVS 847
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Length 1430;
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APPLICANT: Jaffrey, Sanie R.
APPLICANT: Jaffrey, Sanie R.
APPLICANT: Jaffrey, Sanie R.
APPLICANTION: Protein Inhibitor of Neuronal Nitric TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
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Pred. No. 2.6e-50;
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REGISTAATION NUMBER: 32,141
REPERNICE/DOCKET NUMBER: 01107.57071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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1372 LSEEDAGVFISRLRDDNRYHEDIF 1395
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APPLICATION NUMBER: 08/705,625
FILING DATE: 30-AUG-1996
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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Sequence 4, Application US/09123708
Patent No. 6146887
                                                                                        GENERAL INFORMATION:
APPLICANT: SCHRADER, Juergen
APPLICANT: GOEDECKE, Axel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1433
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   US-09-123-708-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHLEIEL--PKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDA---SQQIRLEAEEEK-- 734
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                  APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
RELECOMMUNICATION INFORMATION:
TELEPONE: (415) 324-0960
INFORMATION FOR: SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1433 amino acids
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1374 GKLSAEDAGVFISRMRDDNRYHEDIF 1399
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Best Local Similarity 28.0%; Pr
Matches 192; Conservative 132;
CURRENT APPLICATION DATA:
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963 AFSRMPNQPKTYVQHVMEQDGKKLI--ELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020
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TITLE OF INVENTION: DAM EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REPERENCE: 51169-2003
CURRENT APPLICATION NUMBER: US/09/123,708
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER FILING DATE: 1996-07-03
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1996-03-01
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EARLIER FILING DATE: 1996-03-01
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1315 AYSREPDKPKKYVQDILQEQLAESVYRALKEQGGHIYVCGDVTMAADVLKA-IQRIMTQQ 1373
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Fatent No. 6149936

GENERAL INFORMATION

APPLICANT: SCHRADER, Jurgen

APPLICANT: GODECKE, Axel

TILLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

TILLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

TILLE REFERENCE: 51169-2004

CURRENT PAPLICATION NUMBER: US/09/123,624

CURRENT FILING DATE: 1998-07-28

PRIOR PILICATION NUMBER: 08/553,503

PRIOR PLILING DATE: 1998-03-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN VET: 2.1

SOFTWARE: PATENTIN VET: 2.1

SOFTWARE: PATENTIN VET: 2.1
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1374 GKLSAEDAGVFISRMRDDNRYHEDIF 1399
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ORGANISM: Homo sapiens
US-09-123-624-4
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Best Local Similarity
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457 GIPSPSTEQSAKKVRKKAE------NAHNTPLLVLYGSNMGTAEGTARDLADIA 504
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Therapeutic Constructs
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350 Cambridge Avenue, Suite 250
                                                                      1374 GKLSAEDAGVFISRMRDDNRYHEDIF 1399
1021 HQVSEADARLWLQQLEEKGRYAKDVW 1046
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APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08880342 Patent No. 6218179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
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COMPUTER: IBM PC compatible
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REGISTRATION NUMBER: 38 615
REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 324-0880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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ADDRESSEE: Dehlinger
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SOFTWARE: PatentI
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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23; 504 781 547 841 581 897

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1077 ALGVISNWTDELRLPPCTIFQAFKYYLDITTPPTPLQLQQFASLATSEKEKQRLLVLSKG 1136
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                                                                                                                                                                                                                                                                                                                                                                                                                               457 GIPSPSTEQSAKKVRKKAE------NAHNTPLLVLYGSNMGTAEGTARDLADIA
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                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                         Indels 104;
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                                                                                                                                                   Length 1434;
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APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
                                                                                                                                                Query Match 12.4%; Score 675; DB 2; L
Best Local Similarity 28.0%; Pred. No. 4.9e-50;
Matches 192; Conservative 132; Mismatches 258;
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1375 GKLSAEDAGVFISRMRDDNRYHEDIF 1400
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ADDRESSEE: Dehlinger & Associates
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                                                        MOLECULE TYPE: protein
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APPLICANT: Webster
                                                              ; MOLECULE TYP)
US-08-365-486A-19
                               TOPOLOGY:
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US-08-880-342-19
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582 PAF---IDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNL--DIENSE 636
                                                        CAFGHAVDTLLEELGGERILKMREGDELCGGEEAFRTWAKKVFKAACDVFCVGDDVNIEK
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                                                                                                                 DNKSTLS-------LQFVDSAADMP--LAKMH--GAFSTNVVASKELQQPGSARST
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APPLICANT: Bishoprio, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
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STREET: 350 Cambridge Avenue, Suite 250
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NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/POCKET NUMBER: 8255-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1434 amino acids
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CORRESPONDENCE ADDRESS:
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1197 VAIVSYRTRDGEGPIHHGVCSSWLNRIQADELVPCFVRGAPS-FHLPRNPQVPCILVGPG 1255
                                                                                                                         963 AFSRMPNQPKTYVQHVMEQDGKKLI--ELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020
                                                                                                                                               905 TGVAPFRGFVQARK-QLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGII-TLHT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    723 GTNGTPTKRRAIGFKKLAEAVKFSAKLMGQAMAKRVKATILYATETGKSQAYAKTLCEI- 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     842 ERKSYKVRFNSVSSYSDSQKSSGDGPDLRDNFESAGPLANVRFSVFGLGSR----AYPHF 897
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                                                                      457 GIPSPSTEQSAKKVRKKAE-------NAHNTPLLVLYGSNMGTAEGTARDLADIA
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Snyder, Solomon n. APPLICANT: Snyder, Solomon n. APPLICANT: Jaffrey, Samie R. TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric TITLE OF INVENTION: Oxide Synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.4%; Score 675; DB 2; L
Best Local Similarity 28.0%; Pred. No. 5.6e-50;
Matches 192; Conservative 132; Mismatches 258;
                                                                                                                                                                                                        1021 HQVSEADARLWLQQLEEKGRYAKDVW 1046
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1375 GKLSAEDAGVFISRMRDDNRYHEDIF 1400
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                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08705625 Patent No. 5908756 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-AUG-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
ANME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Banner & Witcoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANÍSM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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ZIP: 20001-4597
COMPUTER REAPABLE FORM:
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TITLE OF INVENTION: OXIG
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   681
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782 FKHAFDAKVMSMEEYDIVHLEHETLVLVVTSTFGNGDPPENGEKFGCALMEMRHPNSVQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                682 RHLEIEL -- PKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDA---SQQIRLEAEEEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 637 DNKSTLS------LQFVDSAADMP--LAKMH--GAFSTNVVASKELQQPGSARST
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4.9e-50;
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                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%; Score 675; 28.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995.
PRIOR APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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Best Local Similarity
Matches 192; Conserv
                     Palo Alto
                                                                                                                                                                                                                                                 FILING DATE: 23
CLASSIFICATION:
                                                                                 94306
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582 PAFIDETLAAKCAENIADRGEADASDDFEGTYEEWREHWWSDVAAYFNLDIENSE 636	17 DNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQQPGSARST 681	12 RHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEK 734	735LAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE- 785	786 KQAYKEQVLAKRITMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASIT 845	6 VSVVSGEAWSGYGE-YKGIASNYLAELQEGDFITCFISTPQSEFTLEKDPETPLINVGPG 904	)5 TGVAPFRGFVQARK-QLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGII-TLHT 962	33 AESRMPNOPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAFAVEATLMKSYADV 1020	1021 HQVSFADARLWLQQLEEKGRYAKDVW 1046
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Search completed: May 29, 2003, 08:22:44 Job time : 24 secs

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May 29, 2003, 08:22:16; Search time 30 Seconds (without alignments) 3536.081 Million cell updates/sec
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Sequence 13, ?
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5457
1 TIKEMPQPKTFGELKNLPLL.......RLWLQQLEEKGRYAKDVWAG 1048
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/cgn2_6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptcdata/2/pubpaa/NS06_NEW_PUB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptcdata/2/pubpaa/PS08_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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## ALIGNMENTS

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Sequence 23, Application US/09371347

Publication No. US20030082676a1

GENERAL INFORMATION:

APPLICANT: ROY A. Gravel et al.

TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:

TITLE OF INVENTION: LOUNING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE

TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER

TILE APPLICATION NUMBER: US/09/371,347

CURRENT APPLICATION NUMBER: US/09/371,347

CURRENT APPLICATION NUMBER: 09/071,622

PRIOR FILING DATE: 1999-01-16

PRIOR FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 51

SOUTHARE FEASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 FVVKAKSKKIP----LGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLYGSNMGTAEGTAR 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499 DLADIAMSKGFAPQVATLDSH----AGNLPREGAVLIV--TASY-NGHPPDNAKQFVDWL 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 RLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDNALVVFCMATYGEGDPTDNAQDFYDWL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 DQASADEVKGVRYSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASDD 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                609 FEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQF----ADMPLAKMH-- 659
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14.0%; Score 766; DB 9; Length 677;
Best Local Similarity 32.4%; Pred. No. 8.1e-48;
Matches 211; Conservative 113; Mismatches 264; Indels
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US-09-371-347-23
US-09-371-347-23
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TYPE: PRT
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Sequence 118,

US-10-139-031-118

Sequence Sequence

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                                               272 OKPPFDAKNPFLAAVTINRKLNO-GTERHLMHLELDISDSKIRYESGDHVAVYPANDSAL 330
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                              ----GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNYEGI 710
                                                                                                                                                                                                       823 SIRPRYYSISSSPRYDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT---- 876
                                                                                                                                                                                                                         711 VNRVTARFG--LDASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMA 768
                                                                                                                                                                                                                                                                                                                           RSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAH 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 LEEDFITWREQFWPAVCEHFGVEATGEESSIRQYELVVHTDIDAAKVYMGEMGRLKSYEN 271
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                                                                                                                                                                                                                                                                 877 ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGC
                                                                                                                                               AKTVCPPHKVELEALLE-----KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLP
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009 US CIP
CURRENT APPLICATION NUMBER: US/09/765,873A
CURRENT FILING DATE: 2001-01-19
PRIOR PEDICATION NUMBER: US 60/147,719
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: MICROSOft Office 97
SEQ ID NO 14
LENGTH: 588
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Matches 189
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APPLICANT: Vogels, Ronald V.
APPLICANT: Vogels, Ronald V.
APPLICANT: Vogels, Refan F.F.
TITLE OF INVENTION: Gene therapy for enhancing and/or inducing anglogenesis
FILE REFERENCE: 2183-5233US
CURRENT APPLICATION NUMBER: US/10/224,249
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: PCT/NLO0/00482
PRIOR APPLICATION NUMBER: EP 99202263.2
PRIOR APPLICATION NUMBER: US 99202263.2
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: US 60/143,101
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EEAEKLIGLPADTYFSLHIDNEDGTPLGGPTLQPPFPPCTLRKALTNYADLLSSPKKSTL 299
                                                                                                                                                                                    821 LPSIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNY-----LAELQEG 874
                                                                                                                                                                                                                                                                                                            875 DTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYF 934
                                                                                                                                                                                                                                                                                                                                                                                                                                       GCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQG 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 GCRNRKVDFIYENELNNFVENGALSELDMAFSR-EGASKEYVQHKMSQKASDIWNMLSEG 535
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                                                             765 RAMAAKTVCPPHKVELEALLE---KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-AL
                                                                                                                                                                                                                        SAAPIFVRT--SNFRLPADPKVPVIMIGPGTGLAPFRGFLQERLALKESGTELGQSILFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1433;
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Best Local Similarity 28.0%; Pred. No. 1.2e-40;
Matches 192; Conservative 132; Mismatches 258;
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OTHER INFORMATION: Human nitric oxide synthase US-10-224-24-9-14
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Publication No. US20030087867A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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--- KLAHLPLAKTVSVEEL 749

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Sequence 13, Application US/10224249

Publication No. US20030087867A1

GENERAL INFORMATION:
APPLICANT: Vogels, Ronald V.
APPLICANT: Vorlinden, Stefan F.F.
TILE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis
FILE REPERENCE: 2183-5233US
CURRENT PILING DATE: 2002-08-19
FRIOR APPLICATION NUMBER: PCT/NL00/00482
PRIOR APPLICATION NUMBER: PCT/NL00/00482
PRIOR PLING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                             KLIELL--DQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYA 1042
                                                                                                                                     SADEVKGVRYSVFGCGDKNWATTYQKVPAF---IDETLAAKGAENIADRGEADASDDFEG 611
                                                                                                                                                                                                             LAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQAR-KQLKEQGQS
                                                                                            HIGIFPGNQTALVQGILERV-VDCPTPHQTVCLEVLDESGSYWVKDKRLP---PCSLSQA
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                                                                      LQY-VELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYP
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CTHER INFORMATION: Homo sapiens inducible nitric oxide synthase US-10-224-249-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.9%; Score 650; DB 9; Length 11:
Best Local Similarity 30.3%; Pred. No. 5.9e-39;
Matches 195; Conservative 112; Mismatches 272; Indels
 HLGVIPRNYEGIVNRVTARFGLDA---SQQIRLEAEEE---
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EDIF 1122
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Batent No. US20020177551A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILLING DATE: 2002-01-14
PRIOR PILLING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 124
LENGTH: 1144
                                                                                                                                                                                                                            AFSRMPNQPKTYVQHVMEQDGKKLI--ELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020
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                         957 ANNSLISNDRSWKRNKFRLTFVAEAPELIQGLSNVHKKRVSAARLLSRQNLQSPKSSRST
                                                                    RHLEIEL--PKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDA---SQQIRLEAEEEK--
                                                                                                                                        -----LAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HQVSEADARLWLQQLEEKGRYAKDVW 1046
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                                                                                             554 AWDLGAL-FSCAFNPKVVCMDKYRLSCLEEERLLLVVTSTFGNGDCPGNGEKLKKSLFML 612
                                                                                                                                            555 SADEVKKVRYSVFGCGDKNWATTYQKVPAF---IDETLAAKGAENIADRGEADASDDFEG 611
                                                                                                                                                                             613 KELNNK-FRYAVFGLG----SSMYPRFCAFAHDIDQKLSHLGASQLTPMGEGDELSGQED 667
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                                                 497 ARDLADIAMSKGFAPQVATLDSH-AGNLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQA 554
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; OTHER INFORMATION: Human nitric oxide synthase
US-10-224-249-15
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Publication No. US20030087867A1
GENERAL INFORMATION:
APPLICANT: Vogels, Ronald V.
APPLICANT: Vogels, Ronald V.
TITLE OF INVENTION: Gene therapy for enhancing the REFERENCE: 2183-5233US
CURRENT FILING DATE: 2002-08-19
PRIOR PILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
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SEQ ID NO 15
LENGTH: 1203
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  507 RPKRREIPL---
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613 KELNNK-FRYAVFGLG----SSMYPRFCAFAHDIDQKLSHLGASQLTPMGEGDELSGQED 667
                                                                                                                                          H--GAFSTNVVASKELQQPGSARSTRHLEI--ELPKEASYQEGDHLGVIPRNYEGIVNRV 714
                                                                                                                                                                        TARF -- GLDASQQIRLEAEEEKLAHLPLAKTV -- - SVEELLQY - VELQDPVTRTQLRAMA 768
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                                                                                           568 AFRSWAVQTFKAACETFDVRGKQHIQIPKLYTSNVTWDPHHYRLVQDSQPLDLSKALSSM 727
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APPLICANT: Tzeng, Edith
APPLICANT: Nussler, Andreas K.
APPLICANT: Geller, David A.
APPLICANT: Simmons, Richard K.
APPLICANT: Shamons, Richard K.
TTLE OF INVENTION: Inducible Nitric Oxide Synthase Gene for Treatment of TITLE OF INVENTION: Disease
                                              TYEEWREHMWS-----DVAAYFNLDIENSEDNKSTLS---LQFVDSAADMPLAK----M
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CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/1/6,496
PRIOR PILING DATE: 1998-10-21
PRIOR FILING DATE: 1995-06-05
PRIOR PILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-06-05
PRIOR PAPLICATION NUMBER: 08/314,917
PRIOR FILING DATE: 1994-09-28
PRIOR PRIOR DATE: 1994-10-28
PRIOR PILING DATE: 1992-11-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
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; ORGANISM: Induced Human Hepatocyte RNA
US-09-992-056-2
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Patent No. US20020061862A1
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APPLICANT: Billiar, Timothy R.
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                                                                                                                                                                                                                                                 Length 679
                                                                                                                                                                                                                                                                      Best Local Similarity 27.2%; Pred. No. 1.8e-35;
Matches 188; Conservative 130; Mismatches 282; Indels
                                                                                                                                                                                                                                                 Score 598; DB 9;
Pred. No. 1.8e-35;
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 117
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; Sequence 117, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
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                                                                                                                                                                                   ; ORGANISM: CANDIDATROPICALIS
US-10-138-838-117
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
                                                                                                                                          LENGTH: 679
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TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
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                                                                                                                                                            ADIAMSKGFAPQVATLDSH-AGNLPREGAVLIVTASY-NGHPPDNAKQFV------ 548
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                                                                       454 PLGGIPSPSTEQSAKKVRKKAEN-------AHNTPLLVLYGSNMGTAEGTARDL
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598 NSSPRPEQHKSYKIRFNSISCSDPLVSSWRRKRKESSNTDSAGALGTLRFCVFGLGSR--
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        al Similarity 26.7%; Pred. No. 7e-36;
191; Conservative 115; Mismatches 254; Indels 155;
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CURRENT APPLICATION NUMBER: US/10/138,838
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Publication No. US20030049821A1
GENERAL INFORMATION:
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: AMdduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
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Loper, John C.
        Best Local Similarity
Matches 191; Conserv
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APPLICANT:
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Gleesno, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
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      648 KIVAKSREISEDKAAELVKSWKVQNRYQEDVW 679
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Matches 188; Conservative 130; Mismatches
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
                                                                                                                                                                         Application US/10138905
5. US:0030068800A1
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Brenner, Alfred A.
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                                                                                                                                                                                                                                                                                                                                         Eirich, Dudley
Eshoo, Mark
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                                                                                                                  APPLICANT: LOPEY, JOHN C.
APPLICANT: LOPEY, JOHN C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOCXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: CYTOCHROME P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX (TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REPERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,031
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
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      Krishna M.
Madduri, Krishna M
Cornett, Cathy A.
Brenner, Alfred A.
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                                                                                                    Tang, Maria
Loper, John C.
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LENGTH: 679
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Glesson, Marin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOR
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
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      PLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEE-LENAQSE 955
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FGSQTGTAEDYANKLSRELHSRFGLKTMVADFADYDWDNFGDITEDILVFFIVATYGEGE
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5 KLDLYVIITLVVAVAAYFAKNQFLDQPQDTGFLNTDSGSNSRDVLSTLKKNNKNT--LLL
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                                                                                             EELLQ-YVELQDPVTRTQLRAMAAKTVCPPHKVELEALL----EKQAYKEQVLAKRLTML
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CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
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APPLICANT: Brenner, Alfred A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDU
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDU
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION NUMBER: US/10/138,916
CURRENT APPLICATION NUMBER: US 09/302,602
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 117
LENGRALE.
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   RPVTGVVTNLLKNVEIVQNKTGEKPLVHYDLSGPRGKFNKFKLPVHVRRSNFKLPKNSTT 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 117, Application US/10138916
Publication No. US20030073220A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Elrich, David L.
APPLICANT: Elrich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Concett, Cathy A.
APPLICANT: Brenner, Alfred A.
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; ORGANISM: CANDIDATROPICALIS
US-10-138-905-83
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LENGTH: 679
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                                                                                                                                                                                                                                                                                                                                                                                                      S. | | | : : : | | | : : : | DSQVSLGEPNKKYINSEGIDLTKG-PFDHTH-PYLARITETRELFS-SKDRHCIHVEFDI 291
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                                                                                                             Length 679;
                                                                                                          Query Match 10.9%; Score 597; DB 9; L. Best Local Similarity 27.2%; Pred. No. 2.1e-35; Matches 188; Conservative 130; Mismatches 282;
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Publication No. US20030068800A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Eirich, Dudley
APPLICANT: Eirich, Dudley
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
            PatentIn version 3.1
                                                                ; ORGANISM: CANDIDATROPICALIS
US-10-139-031-83
NUMBER OF SEQ ID NOS: 118
            SOFTWARE: PA
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Glesson, Maria
APPLICANT: Green C. Maria
APPLICANTION: CANDOREDUCTASE
ATTLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
APPLICANTION: TROPICALIS AND METHODS RELATING THERETO
CURRENT APPLICATION NUMBER: US/10/138,905
CURRENT APPLICATION NUMBER: US/09/976,800
PRIOR PELING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
AND APPLICATION NUMBER: US/09/976,800
APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597 IADRGEADASDDFEGTYEE ----WREHMWSDVAAYFNLD-----
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Search completed: May 29, 2003, 08:27:08 Job time : 35 secs

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Scoring table:

OM protein

Run on:

Minimum DB Maximum DB

Database

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APPLICANT: BLEISS, Juergen
APPLICANT: SCHWANEBERG, Ulrich
APPLICANT: SCHWATT, Jutta
APPLICANT: SCHWATT, Jutta
TITLE OF INVENTION: Novel cytochrome P450 monooxygenases and their use for the oxi
TITLE OF INVENTION: organic substrates
FILE REFERENCE: 50915
CURRENT APPLICATION NUMBER: US/10/031,146
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-27
PRIOR PILING DATE: 2000-07-27
SOFTWARE: Word Perfect version 6.1
SEQ ID NO 2
                                                                               Sequence 4, Appli
Sequence 7, Appli
Sequence 139768,
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Sequence 5, Appli
Sequence 4, Appli
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Sequence 3, Appli
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Sequence 10, Appli
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Sequence 3, Appli
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Sequence 12987, A
Sequence 56962, A
Sequence 118779,
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5 US-10-125-640-2

6 US-10-201-213-2

0 US-10-018-730A-4

0 US-10-018-730A-4

0 US-10-018-730A-4

0 US-10-018-730A-4

0 US-10-105-640-7

0 US-10-125-640-7

0 US-10-125-640-7

0 US-10-125-640-7

1 US-09-71-537-139586

1 US-09-71-537-146499

2 US-08-08-11954-10

2 US-08-09-71-537-105974

4 US-10-021-425-55

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1 US-09-791-537-10974

1 US-09-791-537-10974

1 US-09-791-537-108779
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APPLICANT: Brundard
APPLICANT: Schwaid, Rolf D.
APPLICANT: Schwaneberg, Ulrich
TITLE OF INVENTION: CONVERSION OF SUBStrates
FILE REFERENCE: WA40076
CURRENT APPLICATION NUMBER: US/10/031,241
CURRENT FILING DATE: 2002-05-06
PRIOR PILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 355 В Query Match 100.0%; Score 5457; Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches 661 721 g ò Page 3

361 HRDKTIWGDDVEEFRPERFENPSALPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH  11111111111111111111111111111111111	GEADASDDFEGTYEERREHMASDVAAYPILDIENSEDNKSTLSIQFVDSAADMPLAKMIG  AFSTNVVASKELQOPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRYTARFGL	DD   841 QASITVSVVSGEAMSGYGEYKGIASNYLABLQEGDTITCFISTPQSEFTLPKDPEFPLIM 900	RESULT 4 PCT-US02-11954-2 ; Sequence 2, Application PC/TUS0211954 ; GENERAL INFORMATION: Patrick C. ; APPLICANT: Cirino, Patrick C. ; APPLICANT: ALTOIG, Frances H. ; TITLE OF INVENTION: PEROYIDB-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS ; FILE REFERENCE: 4058/ZK237-W00 CURRENT APPLICATION NUMBER: PCT/US02/11954 ; CURRENT PILING DATE: 2002-04-16 ; PRIOR FILING DATE: 2001-04-16 ; PRIOR FILING DATE: 2001-04-16 ; PRIOR FILING DATE: 2001-05-03 ; PRIOR FILING DATE: 2001-12-12 ; NUMBER FO SEQ ID NOS: 12 ; SOFTWARE: Patentin Version 3.1 ; SEQ ID NO 2 ; LENGTH: 1049 ; TENETH: 1049 ; TUBLICATION INFORMATION: ; PUBLICATION INFORMATION:
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RESULT 5
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P14779
NUMBER: Genbank
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DATABASE ACCESSION NUMBER: GenBa
DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(1049)
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                                Query Match 100.0%;
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMMNSIONAL STRUCTUR
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
LENGTH: 1049
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s; Pred. No. 0;
0; Mismatches
                                                      HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
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llarity 100.0%;
Conservative 0;
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US-09-791-537-53927
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DD 182 LDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG	QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNBHVLQKAAEEAARVLVD 	Qy 301 PVPSYKQVKOLKYVGMYLNEALRIMPTAPAFSLYAKEDTVLGGEYPLEKGDELMYLIPQL 	Qy 361 HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQOFALHEATLVLGMMLKH 	QY 421 FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIBSPSTEGSAKKVRKKAENAHNT 11	QY 481 PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP	Qy 541 PDNAKQEVDWLDQASADEVKGYRYSVEGCGDKNWATTYQKVPAFIDETLAAKGAENIADR	OY 601 GEADASDDFEGTYEEWREHWWSDVAAYFNLDIENSEDRKSTLSLOFVDSAADMPLAKMIG	Qy 661 AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 	Qy 721 DASQOIRLEAEBEKLAHLPLAKTVSVEELLQYVELQDPVIRTQLRAMAAKTVCPPHKVEL 	Qy 781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK 	QY 841 QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM	QY . 901 VGPGTGVAPFRGFVQARKQLKEOGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL	QY 961 HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYIGGDGSQWAPAVEATLMKSYADV	Qy 1021 HQVSEADARLWLQQLEEKGRYAKDVWAG 1048 	S-10-125-640-2 S-10-125-640-2 Sequence 2, Application US/10125640 GENERAL INFORMATION: APPLICANT: CITING, PARTICK C. APPLICANT: Arnold, Frances H.	; FILE REFERENCE: 4058/IK237-US. ; FILE REFERENCE: 4058/IK237-US. ; CURRENT APPLICATION NUMBER: US/10/125,640 ; CURRENT FILING DATE: 2002-04-16 ; PRIOR APPLICATION NUMBER: 60/284,215 ; PRIOR FILING DATE: 2001-04-16 ; PRIOR PPLICATION NUMBER: 60/284,215 ; PRIOR APPLICATION NUMBER: 60/288,636
Qy 601 GEADASDDFEGTYEEWREHWWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 660 Dh 602 GEADASDDFORDSHANGDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 660	661	721 DASQOIRLEABEBEKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 722 DASGOIRLEABEBEKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 722 DASGOIRLEABEBEKLAHLPLAKTVSVEELIQYVELQDPVTRTOLRAMAAKTVCPPHKVEI 722 DASGOIRLEABEBEKLAHLPLAKTVSVEELIQVVELGDPVTRTOLRAMAAKTVCPPHKVEI	781 EALLEKQAYKEQVLAKRITMLELLEKYPACEMKESEFIALIPSIRPRYSISSSERVDEK	QASITYSVYSGEAWSGYGEYKGIASNYLAELQEGDIITCFISTPQSEFTLPKDPETPLIM	VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL	961 HTAFSRMPNOPRITYVQHVMEQDGRKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV	1021 HQVSEADARLWLQQLEEKGRYAKDVWAG 1048	9 Ins.	US-10-03-140-9 Sequence 9, Application US/10031146 GENERAL INFORMATION: APPLICANT: HADER, Bernhard	APPLICANT: PLEISS, Udergen APPLICANT: SCHWANBERG, Ulrich APPLICANT: SCHMITT, Jutta TITLE OF INVENTION: NOVEL CYLCHCOME P450 monooxygenases and their use for the oxidat	FILE REFERENCE: 50915 CURRENT APPLICATION NUMBER: US/10/031,146 CURRENT FILING DATE: 2002-04-30 DPICE ADDITION NUMBER: DOMINGEN	PRIOR FILING DATE: 2000-07-27 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Word Perfect version 6.	; LENGTH: 1049 ; TYPE: PRT ; ORGANISM: Bacillus megaterium fis-10-01-146-0	Ouery Match 100.0%; Score 5457; DB 24; Length 1049; Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY         1 TIKEMPOPKTFGELKNLPLLANTDKPVQALMKIADELGEIFKFEAPGRYTRYLSSQRLIKE 60           Db         2 TIKEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRYTRYLSSQRLIKE 61           QY         61 ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMY 120           Db         62 ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMY 120	121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMYRA 121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMYRA 122 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMYRA 181 LDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG

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EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK
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Best Local Similarity 100.
Matches 1048; Conservative
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P14779
DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(1049)
                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                 100.0%; Score 5457; 100.0%; Pred. No. 0;
        PRIOR APPLICATION NUMBER: 60/340,602
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1049
PRIOR FILING DATE: 2001-05-03
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                     VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
                                                                                                                   2 TIKEMPQPRIFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
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APPLICANT: Farinas, Edgardo
APPLICANT: Glieder, Anton
APPLICANT: Glieder, Anton
APPLICANT: Glieder, Anton
APPLICANT: Arnold, Frances
APPLICANT: Arnold, Frances
APPLICANT: Schwanberg, Ulrich
TITLE OF INVENTION: IMPROVED CYTOCHROME P450 OXYGENASES
FILE REFERENCE: 3369/JK238-US2,
CURRENT APPLICATION NUMBER: US 60/306,766
PRIOR APPLICATION NUMBER: US 60/306,766
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.1
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100.0%; Pred. No. 0;
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DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(1049)
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                                                 Score 5449; Di
Pred. No. 0;
0; Mismatches
       NAME/KEY: MUTAGEN
LOCATION: (1)..(1049)
COTHER INFORMATION: Coding sequence
US-09-856-339A-21
                                                 Query Match
Best Local Similarity 99.8%;
Matches 1046; Conservative
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APPLICANT: Bell, Stephen
FILE REFERENCE: HO-P02196USO (10104571)
CURRENT APPLICATION NUMBER: US/09/0856,339A
CURRENT FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: PCT/GB99/03873
PRIOR APPLICATION NUMBER: GB 9825421.2
PRIOR PILING DATE: 1998-11-19
NUMBER: F SEQ ID NOS: 23
SEQ ID NO 21
LENGTH: 1049
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ORGANISM: Bacillus megaterium
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GENERAL INFORMATION:
APPLICANT: CLIINO, PATILICA C.
APPLICANT: ALNOIG FRANCES H.
TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
FILE REFERENCE: 4058/28237-W00
CURRENT APPLICATION NUMBER: PCT/US02/11954
CURRENT FILING DATE: 2002-04-16
PRIOR PRICATION NUMBER: 60/284,215
PRIOR APPLICATION NUMBER: 60/284,516
PRIOR PELING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-03
PRIOR PELING DATE: 2001-05-03
PRIOR FILING DATE: 2001-10-12
NUMBER OF SED ID NOS: 12
NUMBER OF SED ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
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Best Local Similarity 59.5%; Pred. No. 1e-287;
Matches 628; Conservative 156; Mismatches 259;
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DATABASE ACCESSION NUMBER: Genbank / 008394
DATABASE ENTRY DATE: 2001-10-16
RELEVANT RESIDUES: (1)..(1061)
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                                                                                                                                                                              Sequence 4, Application US/10018730A
GENERAL INFORMATION:
APPLICANT: Luet, Wong
TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS
FILE REFERENCE: P02353013, / 10112404 / N.76277B
CURRENT APPLICATION NUMBER: US/10/018,730A
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 12999-06-18
PRIOR APPLICATION NUMBER: PCT/GB00/02379
PRIOR APPLICATION NUMBER: PCT/GB00/02379
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 18
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Pred. No. 0;
0; Mismatches
                                                                         1021 HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
                                                                                           1022 HQVSEADARLWLQQLEEKGRYAKDVWAG 1049
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US-10-018-730A-4
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Best Local Similarity 99.8%;
Matches 1046; Conservative
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PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
      FILE REFERENCE: 4058/ZK377-WO0
FILE REFERENCE: 4058/ZK377-WO0
CURRENT APPLICATION NUMBER: PCT/US02/11954
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/284,215
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 7
                                                                                                                                               ORGANISM: Bacillus subtilis PUBLICATION INFORMATION:
 ANT: Arnold, Frances
OF INVENTION: PEROXIDE
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Best Local Si
Matches 628;
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MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSD-DLLTHMLNGKDP
                                                                         ETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPVP
                                                                                                           KTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKHFDF
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RESULT 12
PCT-USO2-11954-7
Sequence 7, Application PC/TUSO211954
SERNERAL INFORMATION:
APPLICANT: Cirino, Patrick C.

é 124 126 QLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEA 184 186 243 246 303 306 363 366 423 486 535 546 595 909 654 999 LAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRV 714 EDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSA---KKVRKKAENA--- 477 64 99 GLNNRPLLVLYGSDTGTAEGVARELADTASLHGVRTKTAPLNDRIGKLPKEGAVVVTSS SYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRD YNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAE SRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMVDIAV MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSD-DLLTHMLNGKDP --HNTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTAS NIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDI-ENSEDNKSTLSLQFVDSAADMP KTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKHFDF 5 MPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKEACDE Gaps 12; Length 1061; Indels 259: ch 60.7%; Score 3314; DB 1; 11 Similarity 59.5%; Pred. No. 1e-287; 628; Conservative 156; Mismatches 259; DATABASE ACCESSION NUMBER: GenBank / D69799
DATABASE ENTRY DATE: 2000-07-28
RELEVANT RESIDUES: (1)..(1061) 969 209 655 ŏ g δ

. LARSYEASHASIAENRELQSADSDRSTRHIEIALPPDVEYQEGDHLGVLPKNSQTNVSRI	g :	TYKQVLELTYIRMILNESLRLWPTAPAFSLYPKEDTVIGGKFPITTNDRISVLİPQLHRD
/15 TARKGLDASQQIKLEAEEEEKLAHLPLAKIVSVEELLQY-VELQDPVTRTQLRAAAAKIVC 773 	oy Ob	364 KTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKHFDF 423 367 RDAWGKDAEBFRPERFEHQDQVPHHAYKPFGNGQRACIGMQFALHEATLVLGMILKYFTL 426
774 PPHKVELEALLEKQAVKEQVLAKRLTMLELLEKYPACEMKFSEFIALLESIRPRYYSISS 833 	Qy Db	424 EDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEGSAKKVRKKAENA 477 
834 SPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLFKD 893 	Qy	478HNTPLLVLYGSNMGTABGTARDLADJAMSKGFAPQVATLDSHAGNLPREGAVLJVTAS 535 :
894 PETPLIMVGPGTGVAPFRGFVQARKOLKEOGOSLGEAHLYFGCRSPHEDYLYQEELENAQ 953      :	oy ag	536 YNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATIYQKVPAFIDETLAAKGAE 595 
954 SEGIITLHTÄFSRMPNOPKTYVOHVMEODGKKLIELLDOGAHFYICGDGSQMAPAVEATL 1013 	oy do	596 NIADRGEADASDDFEGTYEEWREHWWSDVAAYFNLDI-ENSEDNKSTLSLQFVDSAADMP 654 :
1014 MKSYADVHQVSEADARLWLQQLEEKGRYAKDVWAG 1048 	yo, do	655 IAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRV 714   ::  ::  ::  ::  : 667 IARSYEASHASIAENRELQSADSDRSTRHIEIALPPDVEYQEGDHLGVLPKNSQTNVSRI 726
RESULT 13 0S-09-791-537-139768	Qy Dp	715 TARFGLDASQQIRLEAEBEKLAHLPLAKTVSVEELLQY-VELQDPVTRTQLRAMAAKTVC 773 
Sequence 15,708, Application US/US/9153/ GENERAL INFORMATION: APPLICANT: Bionomix, inc. APPLICANT: Debe, Dereck	. Oy	774 PPHKVELEALLEKQAYKEQVIAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISS 833
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210	yo, du	834 SPRVDEKQASITVSVVSGEAMSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKD 893      ::
CORRENT AFFICIATION UNDER: US/09//91,53/ CURRENT FILING DATE: 2001-02-22 NUMBER OF SEQ ID NOS: 153055 SOFTWARE: Patentin version 3.0	Qy	894 PETPLIMVGPGTGVAPFRGFVQARKQLKEGGSLGEAHLYFGCRSPHEDYLYGEELENAQ 953 
TENGTH: 1061	oy Op	954 SEGIITLHTAFSRAPNQPKTYQHVMEQDGKKLIELLDQGAHFYIGGDGSQNAPAVEAL 1013 
Query Match  Query Match  Best Local Similarity 59.5%; Pred. No. 1e-287;  Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;	da .	1014 MKSYADVHQVSEADARLWLQQLEEKGRYAKDVWAG 1048  :        : :   :   :          1026 QKAYQAVHGTGEQEAQNWLRHLQDTGMYAKDVWAG 1060
5 MPQPRTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDE 64 	RESUI US-1	RESULT 14 US-10-125-640-6 ; Sequence 6, Application US/10125640
65 SRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWRKAHNILLFSFSQQAMKGYHAMMVDIAV 124     ::  :  :   :		GENURAL INFORMATION: APPLICANT: CIrino, Patrick C. APPLICANT: Arnold, Frances H. TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
125 QLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEA 184 		; FILE REFERENCE: 4058/1K237-US3 ; CURRENT APPLICATION WUMBER: US/10/125,640 ; CURRENT FILING DATE: 2002-04-16 ; PRIOR APPLICATION NUMBER: 60/284,215
185 MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSD-DLLTHMLNGKDP 243 		IJOR FILING DATE: 2001-04-16 YIOR APPLICATION NUMBER: 60/288,636 YIOR FILING DATE: 2001-05-03 YIOR APPLICATION NUMBER: 60/340,602
244 ETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPVP 303 	PR.	NOR FILING DATE: 2001-12-12 NMBER OF SEQ ID NOS: 12 NFTWARE: PATENTIN VETSION 3.1
304 SYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRD 363 :     :   :  :		LENGTH: 1061 TYPE: PRT ORGANISM: Bacillus subtilis

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US-10-125-640-7
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|LARSYEASHASIAENRELQSADSDRSTRHIEIALPPDVEYQEGDHLGVLPKNSQTNVSRI 726
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                                                               Gaps
                                                               12;
                                                Length 1061;
                                                               Indels
                                             tch 60.7%; Score 3314; DB 25; al Similarity 59.5%; Pred. No. 1e-287; 628; Conservative 156; Mismatches 259;
      DATABASE ACCESSION NUMBER: GenBank / 008394
DATABASE ENTRY DATE: 2001-10-16
RELEYANT RESIDUES: (1)..(1061)
PUBLICATION INFORMATION
                        ; RELEVANT RE:
US-10-125-640-6
                                              Query Match
Best Local S:
Matches 628
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                                                                                                                                                                                                                     Sequence 7, Application US/10125640

GENERAL INFORMATION:

APPLICANT: Cirino, Patrick C.

APPLICANT: Arnold, Frances H.

TITLE OF INVENTION: PEROXIDE-DRIVEN CYTCCHROME P450 OXYGENASE VARIANTS

FILE REFERENCE: 4058/1K237-US3

CURRENT APPLICATION NUMBER: 05/10/125,640

CURRENT APPLICATION NUMBER: 05/284,215

PRIOR APPLICATION NUMBER: 60/284,215

PRIOR PLICATION NUMBER: 60/288,636

PRIOR PLICATION NUMBER: 60/288,636

PRIOR PELING DATE: 2001-04-16

PRIOR PELICATION NUMBER: 60/340,602

PRIOR PELICATION NUMBER: 60/340,602
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                                                                                MKSYADVHQVSEADARLWLQQLEEKGRYAKDVWAG 1048
                                                                                                      1026 QKAYQAVHGTGEQEAQNWLRHLQDTGMYAKDVWAG 1060
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Pred. No. 1e-287;
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DATABASE ACCESSION NUMBER: GenBank / D69799
DATABASE ENTRY DATE: 2000-07-28
RELEVANT RESIDUES: (1)..(1061)
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Best Local Similarity 59.5%; Pro
Matches 628; Conservative 156;
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SOFTWARE: Patentin version 3.1
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:16; Search time 54 Seconds

(without alignments)

4017.377 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457
Sequence: 1 TIXEMPOPKTFGELKNLPLL......RLWLQQLEEKGRYAKDVWAG 1048

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 995812 seqs, 207002235 residues

Total number of hits satisfying chosen parameters: 995812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/paa/USO7\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

		Description	Sequence 24, Appl		Sequence 14954, A							•		.,	_	Sequence 177338,			٠.	14960	Sequence 8116, Ap	8116,	1, App			4	Sequence 86297, A	
SUMMARIES		DI	US-10-214-446-24	US-10-156-761-8117	US-10-156-761-14954	US-10-219-051B-11638	US-10-219-051B-12755	US-10-148-907A-23	US-10-219-051B-12757	US-60-440-068-572	US-10-424-599-187294	US-10-425-114-70174	US-10-424-599-191313	US-10-188-523B-14	US-10-188-523C-14	US-10-424-599-177338	US-09-661-258-2	US-60-452-680-23982	US-60-453-135-14960	US-60-453-050-14960	ч	US-60-465-241-8116	US-09-661-258-1	US-09-751-708A-124	US-09-661-258-5	US-09-661-258-4	US-09-724-676-86297	US-09-724-676A-86297
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de	Query	Match	44.4	35.7	17.5	14.2	14.2	14.1	14.1	14.1	13.3	13.1	13.0	12.9	12.9	12.6	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.2	12.2	12.2	12.1	12.1
		Score	2420.5	1945.5	953.5	777.5	777.5	169	767	167	728.5	712.5	710	705.5	705.5	688	678	675	675	675	675	675	675	665.5	665.5	665	199	199
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 NGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVL 298

187

App			14;	61	121 126	181
5970, 313, 46194, 661914, 7634, 7634, 11109 11109 1110, 83, Ap 111, Ap 111, Ap 111, Ap			Gaps	RLIKEA  ::  OLVEEL	HAMMYD       HPSMYD	SMVRAL
sednence sed		мант	1077; 35;	RYLSSQI :   VIVSGHI	DAMKGYI :11:1 RAMQSYI	PHPFITS
			Length Indels	IKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEA : :	CDESREDKNLSQALKFVRDFAGDGLFTSWTHERNWKRAHNILLPSFSQQAWKGYHAMMVD 	IAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRAL
		ENCODING AND USING al sample		FKFE   : FWLD	HNIL	YREN 
5970 -313 -4154 -6191 -6191 18506 111109 5820 5820 5820 -3 -3 -11 -11 -11 -11 -11 -11 -11 -11 -		11	DB - 202	ELGE1       ELGP1	NWKK?       NWSK?	LCGFN
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2001-08-02

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NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8117
 PRIOR FILING DATE:
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TGVDRTTGEQLDDVNIRYQINTFLIAGHETTSGLLSCTLYALLKHPEILRKAYEEVDRVL 304
                                                                                                                                                                                                                                                                                            HLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEKLAHLPLAKTVSVEELL-QYVELQD 757
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                                                                                                                                               305 GPDINARPTYQQVTQLTXITQILKEALRLWPPAPAYGISPLKDETIGGKYKLKKNTFITV
                                                                                                                                                                         EGAVLIVTASYNGHPPDNAKQFVDWL-DQASADEVKGVRYSVFGCGDKNWATTYQKVPAF
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                   ---VDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMV
                                                         LIPQLHRDKTIWGDDVEEFRPERF--ENPSAIPQHAFKPFGNGQRACIGQQFALHEATLV
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GENERAL INFORMATION:
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APPLICANT: OMURA, SATOSHI
APPLICANT: INEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, YOSHIYOKI
APPLICANT: HATTORI, YOSHIYOKI
APPLICANT: HATTORI, MASAHIRA
TITLE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2001-26-30
PRIOR FILING DATE: 2001-204089
PRIOR FILING DATE: 2001-205-30
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                                                                                                                                                               SSQRLIKEACDESRFDKNLSQA-LKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQA
                                                                                                                                                                                                                                                                                   MKGYHAMMVDIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPH
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                                                                    Length 1073;
                                                                      ;
6
                                                                                                         408;
                                                                  35.7%; Score 1945.5; DB 6
llarity 38.2%; Pred. No. 2.4e-160;
Conservative 195; Mismatches 408;
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8117
                                                                  Query Match
Best Local Similarity
Matches 417; Conserv
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Thu Kay

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HVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLE 1036
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RKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNQPKTYVQ
                                                                                                                                     | :| : : ||| | | | | | :|::: | | :|||| | :|| :|| :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
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43.1%; Pred. No. 3.6e-74;
tive 79; Mismatches 174;
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HINOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNCLEOTIDES
FILE REFERBNCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
SEQ ID NO 14954
LENGHES OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14954, Application US/10156761 GENERAL INFORMATION:
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US-10-156-761-14954
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1063 ADERYQQDVFA 1073
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APPLICANT: The General Hospital Corporation doing business as Massachusetts Genera APPLICANT: Hospital / Bayer AG
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                                                                                                                                                                                                                                                                                                                                                                 AFPLICARY: INCEPTION: Nucleotide sequences involved in pain FILE REFERENCE: LeA 35633 Foreign Countries CURRENT APPLICATION NUMBER: US/10/219,051B CURRENT APPLICATION NUMBER: US 60/312,147
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-11-01
PRIOR PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SEQ ID NO 11638
LENGTH: 677
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ches 263;
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; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-11638
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14.2%; Score 777.5; I
Best Local Similarity 32.2%; Pred. No. 1.6e
Matches 211; Conservative 111; Mismatches
                                                                                                                                                                                                                                         ; Sequence 11638, Application US/10219051B; GENERAL INFORMATION:
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Db 505 RALVPMFVRKSQFRLPFKSTTPVIMVGPGTGIAPFMGFIQERAWLREQGKEVGETLLY 562  Qy 934 FGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNOPKTYVQHVWEQDGKKLIELLDQ 992  :	RESULT 6 US-10-148-907A-23  Sequence 23, Application US/10148907A  Sequence 23, Application US/10148907A  GENERAL INFORMATION:  APPLICANT: NOVATIS AG  TITLE OF INVENTION: Compositions and Methods for Halegenation Reactions  FILE REFERENCE: S-31082A  CURRENT APPLICATION NUMBER: US/10/148,907A  CURRENT FILING DATE: 2002-06-04  PRIOR FILING DATE: 2000-01-03  PRIOR FILING DATE: 2000-01-03  PRIOR FILING DATE: 2000-01-03  SEQ ID NO 23  LENGTH: 682  TYPE: PRT  ORGANISM: Oryctolagus cuniculus	US-10-148-907A-23 Query Match Query Match Best Local Similarity 31.7%; Pred. No. 9e-58; Matches 212; Conservative 111; Mismatches 250; Indels 96; Gaps 24;	QY         444 EVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSNMGTAEGTA 497             : :   : :   : :	DD 100 NRLSKDAHRYGMRGMAADPEEYDLADLSSLPEINNALAVFCMATYGEGDPTDNAQDFYDW 159  QY 551 LDQASADEVKGVRYSVFGCGDKWATTYQKVPAFIDETLAAKGAENIADRGEADASD 607	608 DFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLGFVDSAADMPLAKMH :	Db 272 SYENQKPPFDAKNPFLATVTTNRKLNQ-GTERHLMHLELDISDSKIRYESGDHVAYYPAN 330  Qy 707 YEGIVNRYTARFGLDASQQIRLEAEEEKLAHLPLAKTVSV 746  11:	747 EELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQAYKBQVLAKRLTMLELLEK	Db 438 YPSLRPPIDHLCELLPRLQARYYSIASSSKVHPNSVHICAVAVEYETKAGRLN-KGVATS 496 QY 867 YL-AELQBGDTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQL 920   1
QY         934 FGCRSPHEDYLYOEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEDDGKKLIELLDQ 992           :	Sequence 12755, Application US/10219051B GENERAL INCORMATION: GENERAL INCORMATION: APPLICANT: The General Hospital Corporation doing business as Massachusetts General APPLICANT: The General Hospital / Bayer AG TITLE OF INVENTION: Nucleotide sequences involved in pain FILE REFERENCE: LeA 35633 Foreign Countries CURRENT FILING DATE: 2003-05-09 FRIOR APPLICATION NUMBER: US 60/312,147 PRIOR FILING DATE: 2001-08-14 PRIOR FILING DATE: 2001-10-08-14 PRIOR PRIOR APPLICATION NUMBER: US 60/345,382 PRIOR APPLICATION NUMBER: US 60/333,347 PRIOR FILING DATE: 2001-11-26 NUMBER OF SEQ ID NOS: 14715 SOFTWARE: Perl script SEQ ID NO 12755 LENGTH: 677 TYPE: PRT CORGANISM: Rattus norvegicus	; PUBLICATION INFORMATION: ; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41064 ; DATABASE ENTRY DATE: 2002-06-15 US-10-219-051B-12755 OUETV MATCh	Similarity 31.2%; Pred. No. 1.6e-58; Indels 1; Conservative 111; Mismatches 263; Indels FVVKAKSKKIPLGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLY 1::		Qy         552 DQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDD 608           1	Qy 660GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHJGVIPRNY 707	327 SALVNQIGEILGADLDVIMSLNNLDEESNKKHPFPCPTTYRTALTYYLDITNP-PRINVL 766 AMAARTVCPPHKVELEALLEKQAYKEQVLAKRLIMLELLEKYPACEMKFSEFIA 1:	QY 820 LLPSIRPRYXSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT 876

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 96
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TITLE OF INVENTION: POLYNOLLEDTIDES AND POLYPEPTIDES ASSOCIATED WITH THE TITLE OF INVENTION: POLYPEPTIDES ASSOCIATED WITH THE TITLE OF INVENTION: NF-KB PATHWAY FILE REFERENCE: 3053-4191
CURRENT APPLICATION NUMBER: US/60/440,068
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
                                                                       RSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAH
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                                                   ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGC
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                                                                                                                                                                                                          14.1%; Score 767; DB 7; Length 677; 32.4%; Pred. No. 1.3e-57; Live 113; Mismatches 264; Indels
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Sequence 572. Application US/60440068
SENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
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US-60-440-068-572
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Matches 211;
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LENGTH: 677
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TITLE OF INVENTION: NUclectide sequences involved in pain
FILE REPERRNCE: LeA 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-11-26
NUMBER: OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SEQ ID NO 12757
                                                                 980 EQDGKKLIELLDQ-GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEK 1038
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                                 ROOGKEVGETLLYYGCRRAAEDYLYREELAGFOKDGTLSQLNVAFSREQAQ-KVYVQHLL
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DATABASE ACCESSION NUMBER: SWISS-Prot / BAB18572
DATABASE ENTRY DATE: 2002-06-15
                                                                                                                                                                                                                                                   ; Sequence 12757, Application US/10219051B; GENERAL INFORMATION:
                                                                                                                                   GRYAKDVWA 1047
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GRYSLDVWS 682
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ORGANISM: Homo sapiens
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Oy 902 GPGTGVAPPRGFVQARKQLKEDGOSLGCBAHLYFGCRSPHEDYLYGEELENAQSEGIIT-L 960	Quety Match
DD 509 VPMFVRKSQFRLPFKATTPVIMVGPCTGVAPFIGFIOERAWLROOCKEVGETLLYGC 566  937 RSPHEDYLLYGELENAGSEGITT-LHTAFSRAMPOPKTYVQHVMEDOCKKIJELLDOGAH 995	Query Match         13.3%; Score 728.5; DB 6; Length 689;           Dest Local Similarity 31.2%; Pred. No. 3.2e-56; Indels 73; Gaps 20;           Matches 195; Conservative 102; Mismatches 256; Indels 73; Gaps 20;           PRED. Conservative 102; Mismatches 256; Indels 73; Gaps 20;           QY 80         TPLLVINGSNMGTAGETARDLADGNLPREGALD 530             : : : : : : : : : : : : : : : : : : :

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953 QSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEA 1011
                                                                                                                           765 RAMAAKTVCPPHKVELEALLE----KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-AL 820
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479 FAPQRVHVTCALVYGPTPTG-RIHKGVCSTWMKNAIPLEKSPDCSWAPIFIRPSNFKLPV 537
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                                                     18 DLDDYA------ADDEEYAEKFKETFAFFLATYGDGEPTDNAARFYKWFTEG---
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                                    DPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENA
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TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REPERENCE: BC1009 US DIVCIP
CURRENT APPLICATION NUMBER: US/10/188,523B
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: MICROSOFT Office 97
SEQ ID NO 14
LENGTH: 588
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                                                                                                                                                                                                      RESULT 12
US-10-188-523B-14
; Sequence 14, Application US/10188523B
; GENERAL INFORMATION:
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Best Local Simil
Matches 189; C
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Show Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT FILLS DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191313
                                                                       962 TAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVH 1021
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PGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIIT-LH 961
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                                576 PGTGLAPFRGFLQERLALKQSGAELGTSILFFGCRNRNMDYIYEDELQTFLEEGALSELI
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US-10-424-599-191313
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.larity 28.2%; Pred. No. 1.3e-52;
Conservative 123; Mismatches 288;
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; GENERAL INFORMATION:
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ORGANISM: Glycine max
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196; Conserv
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US-10-424-599-191313
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499 DLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQASAD
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                                    994 AHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVW 1046
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                                                 67;
                                                                                                                   Sequence 14, Application US/10188523C
GENERAL INFORMATION:
GENERAL INFORMATION:
TOTAL OF INTENTION:
FILE REFERENCE: BC1009-CIP
CURRENT PAPLICATION NUMBER: US/10/188,523C
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR PAPLICATION NUMBER: US 09/627,216
PRIOR PELING DATE: 1999-08-06
PRIOR FILING DATE: 1999-08-06
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31.9%; Pred. No. 2.5e-52;
Live 92; Mismatches 245;
                                                                                                                                                                                                                                                                                                                       ORGANISM: Helianthus tuberosus
                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 38
SOFTWARE: MCROSOFT OFFICE 97
SEQ ID NO 14
LENGTH: 588
                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity J. Matches 189; Conservative
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APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Moreovement FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 177338
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: OTHER INFORMATION: unsure at all Xaa locations
: FEATURE:
: OTHER INFORMATION: Clone ID: PAI_MRT3847_131152C.1.pep
US-10-424-599-177338
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                                                 Sequence 177338, Application US/10424599
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovallo David K
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RESULT 14
US-10-424-599-177338
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646 SEIWSMISQGAYIYVCGDAKGMARDVHRALHTILQEQGSLDSSKAESMVKNLQTTGRYLR 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants FILE REFERENCE: 26473/04028
CURRENT APPLICATION NUMBER: US/09/661,258
CURRENT FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                 RESULT 15
US-09-661-258-2
; Sequence 2, Application US/09661258
; GENERAL INFORMATION:
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APPLICANT: Adak, Subrata
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; ORGANISM: Rattus rattus
US-09-661-258-2
                                                                                 1044 DVW 1046
                                                                                                                                            DVW 708
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Db 1372_LSEEDAGVFISRLRDDNRYHEDIF 1395
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Search completed: May 29, 2003, 08:26:31 Job time : 58 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:26:36; Search time 49 Seconds

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2056.099 Million cell updates/sec
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Title:
US-10-031-146-2
Perfect score: 5457
Sequence:
1 TIKEMPQPKTFGELKNLPLL......RLWLQQLEEKGRYAKDVWAG 1048
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283224 segs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Listing first 45 summaries
PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

NADPH-ferrihemopro NADPH-ferrihemopro NADPH-ferrihemopro NADPH-ferrihemopro NADPH-ferrihemopro NADPH-ferrihemopro NADPH-ferrihemopro cytochrome P450 / NADPH-ferrihemopro nitric-oxide synth nitric-oxide synth NADPH-ferrihemopro nitric-oxide synth synth protein K10D2.6 tric-oxide Description SUMMARIES Query Match Length DB Score 761.5 739.5 737.5 735.5 723 723 711.5 705.5 702.5 684.5 683.5 679 Result ٠ 9

nitric-oxide synth	NADPH-cytochrome P	nitric-oxide synth	nitric-oxide synth	nitric-oxide synth	NADPH-ferrihemopro	nitric-oxide synth	nitric-oxide synth	NADPH-ferrihemopro	sulfite reductase	sulfite reductase	NADPH-ferrihemopro	NADPH-ferrihemopro	NADPH-ferrihemopro	nitric-oxide synth	nitric-oxide synth
S47647	JE0230	A43271	JC5028	A49676	S38427	JC5027	S65440	863698	A83726	G70040	S63895	S37156	JC7192	T31331	A47501
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1147	713	1144	1147	1153	693	1147	1147	680	607	605	680	206	710	1247	1203
12.3	12.3	12.2	12.2	12.1	12.0	12.0	12.0	11.7	11.7	11.5	11.5	11.5	11.3	11.3	11.2
671.5	699	665.5	664.5	661	657.5	654.5	654.5	639	636.5	628.5	628	627.5	617.5	614.5	608.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300

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,		akeuchi, M.; Tamakoshi, A.; Tan
	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAREFAARVLVD	T.; Winters, P.; Wipat, A.; Yam A;Authors: Yoshikawa, H.F.; Zum
4y 301 Db 302	PYPEYKOVKOLKYVENYONALDEALKLUMPTAPARSIZAKENTYGGGEPPEKKOLEMYLIPOL 360 	A; Title: The complete genome se A; Reference number: A69580; MUI A; Accession: D69799
0у 361		A; Molecule type: DNA
Db . 362		A; Residues: 1-1061 <kun> A; Cross-references: GB: Z99107;</kun>
0y 421	FOFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480 	A; Experimental source: strain I C; Genetics: A; Gene: yetO
	EDEBUTINEBULLING LULUNGER DOE VVARANDANA FLAGGIFOVO I BUDANA VANAAENAHNI. DI TIT VOCHACAM BUMBADA BAT BALGOVIB BOOLEME BOUL BOOLE ANT BUMBADA TETTA	C; Superiamily: P450 bilunctiona C; Keywords: chromoprotein; flav
Uy 481	FLEVELSCANGIAEGIAROLED LAGGAGE PECVATILISHAGALEREGAVILTTASINGHP 340 	F;264-425/DOmain: Cytochrome P4 F;493-1057/Domain: NADPH-ferrih F;495-632/Domain: flavodoxin ho
Oy 541 Db 542	PDNAKQFVDWIDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR 600 	F;403/binding Sile: neme iron ( Query Match Best Local Similarity 59.5%
Qy 601	GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG	vat
Db 602		Qy 5 MPQPKTFGELKNLPLLN:::t            ::
.Qy 661	AFSTNVVASKELQOPGSARSTRHLEIELPKEASYOEGDHLGVIPRNYEGIVNRVTARFGL 720 	DD / IPOPKTFGPLGNLPLID Oy 65 SRFDKNLSQALKFVRDF
	TA COLTO TERREPORT A UT DI APPRICADET I CAUTE COLTO PARA APPRICADETE ESTA	Β̈́
		. 125
Oy 781 Db 782	EALLEKOAYKEOVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYSISSSPRVDEK 840	Db 127 QLIQKWARLNPNEAVDV Qy 185 WNKLQRANPDDPAYDEN  :::   :
Qy 841	QASITVSVVSGBAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM	187
Db 842		Oy 244 ETGEPLDDENIRYCHIT
	VGPGTGVAPFRGFVQARKQLKEGGGSLGEAHLYFGCRSPHEDYLYGEELENAGSEGIITL	304
	VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL	DD 307 TYKQVLELTYIRMILNE
Qy 961 Db 962	HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020 	
Oy 1021	HQVS	367
Db 1022	HQVSEDARIMIQQLEEKGRYAKDVWAG 1049	UY 424 EDHTNIELDIKETLILK 
RESULT 2		Qy 478HNTPLLVLYGSNMGT
cytochrome P4	150 / NADPH-cytochrome P450 r homolog yetO - Bacillus subtilis	Db 487 GLNNRPLLVLYGSDTGT
C;Date: 05-De C:Accession:	oriting sucritis c-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000 D69799	Qy 536 YNGHPPDNAKQFVDWLDO
R; Kunst, F.; C.; Bron, S.;	Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.: Chd	Db 547 YNGKPPSNAGQFVQWLQI
A.; Ehrlich, Nature 390, 2	S.D.; Emmerson, P.T.; Entian, R.D.; Errington, J.; Fabret, C.; Ferrari, E. 49-256, 1997	596
iech, J.; Har	unger, D.; Filez, C.; Fullea, M.; Fullea, I.; Fuma, S.; Galizzl, A.; Galler wood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.	607
Noetter, P.; A;Authors: La Y, M.; Ogawa,	Noetter, P.; Noningstein, G.; Krogn, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; A.; A.; Lardinois, A.; A.; A.; Liu, H.; Masuda, S.; Maueel A.; A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S. H.; Parro, V.; Pohl, T.M.; Porteteile	QY 655 LAKMHGAFSTNVVASKEI   ::  :::   Db 667 LARSYEASHASIAENREI
Rieger, M.; A;Authors: Sc	Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, hibleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron	Qy 715 TARFGLDASQQIRLEAE
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anaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya anamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida umstein, E.; Yoshikawa, H.; Danchin, A. sequence of the Gram-positive bacterium Bacillus subtili JID:98044033; PMID:9384377 GB:AL009126; NID:92632866; PIDN:CAB12544.1; PID:926330 168 nal enzyme CYP102; cytochrome P450 homology; flavodoxin avoprotein; heme; iron; metalloprotein P450 homology <P45> homology <P45> homology <PEH> homology <PEH> homology <PEX> (Cys) (axial ligand) #status predicted 6 TFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEBAARVLVDPVP 303 243 246 423 535 546 999 184 477 TYEEWREHMWSDVAAYFNLDI-ENSEDNKSTLSLQFVDSAADMP 654 ELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRV 714 EEEKLAHLPLAKTVSVEELLQY-VELQDPVTRTQLRAMAAKTVC 773 acid sequence not shown; translation not shown 64 99 ...ATDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDE ENPSAIPQHAFKPFGNGORACIGQOFALHEATLVLGMMLKHFDF KPEGFVVKAKSKKIPLGGIPSPSTEQSA---KKVRKKAENA---|||| ||:||| | : | |: | |:|||:|||:||:| TAEGVARELADTASLHGVRTKTAPLNDRIGKLPKEGAVVIVTSS **VPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEA** NKRQFQEDIKVMNDLVDKIIADRKASGEQSD-DLLTHMLNGKDP TAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTAS Indels 12; Gaps %; Score 3314; DB 2; Length 1061; %; Pred. No. 5.7e-178; 156; Mismatches 259; Indels 12;

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246 303 306 363 366 423 426 480 484 540 544 900 604 99 664 720 724 779 783 838 843

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NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - rat
N;Alternate names: NADP-cytochrome P450 reductase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 03-Jun-2002
C;Accession: A36073; A00402; A25813
R;Porter, T.D.; Beck, T.W.; Kasper, C.B.

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C; Accession: A25584; A00403
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    Halochanistry 29, 1844-9481, 1990

A) Helcensistry 29, 1844-9481, 1990

A) Helcense number: A36073; MUID:91104888; PMID:2125483

A) Reference number: A36073; MUID:91104888; PMID:2125483

A) Roccust type: DNA

A) Residues: 1-678 CRO25

A) Title: Napple: CL 8.

B) R) Rockers: T. D.; Rasper, CL 8.

A) ATILE: Coding nucleotide sequence of rat NADPH-cytcohrome P-450 oxidoreductase cDNA arrangements And A1 Title: Coding nucleotide sequence of rat NADPH-cytcohrome P-450 oxidoreductase cDNA arrangements AND A1 Title: Coding nucleotide sequence of rat NADPH-cytcohrome P-450 oxidoreductase cDNA arrangements AND A1 Title: Coding nucleotide sequence of rat NADPH-cytcohrome P-450 reductase cDNA arrangements AND A1 Title: Expression and A1 Title: Expression of rat NADPH-cytcohrome P-450 reductase cDNA in Saccharomyces cereving R: Murakani, H.: Yabusaki, Y.: Ohkawa, H.

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Biochemistry 29, '9814-9818, 1990
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A.Wolecule type: protein
A.Residues: 56-162, 'S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A.Residues: 56-162, 'S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
C. Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo
C. Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flav
F; 76-126/Domain: FMN binding <FMN>
F; 76-126/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F; 81-223/Domain: flavodoxin homology <FLX>
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A; Residues: 1-677 <HAN>
R; Vogel, F.; Lumper, L.
Biochem. J. 236, 871-878, 1986
A; Title: Complete structure of the hydrophilic domain in the porcine NADPH-cytochrome
A; Reference number: A00403; MUID:87075664; PMID:3098240
A; Accession: A00403.
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                                                               563
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---ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLY
                                    FGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQ
                                                                                                                                                                                                                                                              -GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPAVCEHFGVEATGEESSIRQYELVVHTDMDTAVVYTGEMGRLKSYENQKPPFDAKNPFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 AVVTTNRKLNQ-GTERHLMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGEILGTDL
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F;1/Modified site: acetylated amino end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Hanlu, M.; Iyanaqi, T.; Miller, P.; Lee, T.D.; Shively, J.E. Biochemistry 25, 7966-7911, 1986
A; Title: Complete anino acid sequence of NADPH-cytochrome P-450 A; Reference number: A25584; MUID:87101085; PMID:3099837
A; Accession: A25584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - pig
N:Alternate names: NADP-cytochrome P450 reductase
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Dec-1986 #sequence_revision 03-Feb-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 677;
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09 780 LEALLEKOAYKROVLAKRIJMLELLEKYPACEMKFSEFIALLESISPRPRYSISSS 814 401 LEKNASSGEGERIETISHWYPARRHILAILOOFSELREPDHICCELLRICARYYSISSS 460 635 PRYDEKOASITVSVVSCEAMSGYCEKKGISKUL-AELDGEDTITCFISTPOSEF 888 461 STUPNSVHICANVLYSCEAMSGYCEKKGISKUL-AELDGEDT	11 NIEBDEITWREDEWPAVCEHFGVEATGEESSIRGYELVLHTDIDVAKYGGEMGRLK 268 660GAFSTWARE GOOGSAFSTRELEEL-PKEASYGGEDHGVIPRY 706 15 SYENGKPPFDAKNPFLATVTTNRKLNG-GTERHLMHLEEDISDSKIRYESGDHVAVYPAN 327 707 YEGIVNRYTARFGLDASGOIRLEAEDEKLAHLDL
F;83-225/Domain: flavodoxin homology <flx> F;85-96/Region: FMN phosphate binding #status predicted F;268-327,453-478/Domain: FAD binding #status predicted <fad> F;294-297/Region: FAD-pyrophosphate binding #status predicted</fad></flx>	Rivanano, S.; Aoyama, T.; McDride, O.W.; Hardwick, J.P.; Gelboin, H.V.; Gonzalez, F.J. Mol. Pharmacol. 36, 83-88, 1989 A.Title: Human NADPH-P450 oxidoreductase: complementary DNA cloning, sequence and vac A; Reference number: A60557; MUID:89313720; PMID:2501655 A.Rocession: A60557
Ouery Match  14.1%; Score 769; DB 2; Length 679;  Best Local Similarity 31.7%; Pred. No. 1.9e-35;  Matches 212; Conservative 111; Mismatches 250; Indels 96; Gaps 24;  444 FVVKAKSKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSNMGTAECTA 497    ::    ::    ::	A;Accession: Acoust A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-137, G', 139-577, DV', 580-677 < YAM> A;Shephard, E.A.; Pelmer, C.N.A.; Segall, H.J.; Phillips, I.R. Arch. Biochem. Biophys. 294, 168-172, 1992 A;Title: Quantification of cytochrome P450 reductase gene expression in human tissues
498 RDLADIAMSKGFAPQVATLDSHAGNIPREGAVLIVTASY-NGHPPDNAKQFVDW 550	A; Accession: S.1080 A; Molecule type: mRNA A; Residues: 2-499, 'v', 501-517, 'L', 519-536, 'WH', 539-677 < SHE> A; Cross references: GB = 8.8904669; NID: 9247306; PID: 130v0doxin homology; NADPH-ferrihemo C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo C; Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flav F; 1-56.70main: membrane-bound % status predicted (ARM> F; 2-677/Product: NADPH-ferrihemoprotein reductase # status experimental < CAMT> F; 77-227/Domain: FMN binding % status predicted < FNN> F; 80-675/Domain: NADPH-ferrihemoprotein reductase homology < FEH>

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NADPH-ferrihemo

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Biochim. Biophys. Acta 1174, 313, 1993
A; Reference number: S38510; MUID:93385164; PMID:8373812
A; Contents: annotation; erratum
C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoforcein reductase; flavodoxin homology; NADPH-ferrihemoforcein reductase; flavodoxin homology; NADPH-ferrihemoprotein reticulum; FAD; flavoprotein; FMN; NADP; F; 99-184 /Domain: FMN binding #status predictase homology <FEH>
F; 80-676 /Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F; 80-224 /Domain: flavodoxin homology <FELX>
F; 82-224 /Domain: flavodoxin homology <FELX>
F; 292-326, 454-477 /Domain: FAD binding #status predicted <FAD>
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A;Residues: 1-692 <BEV>
A;Cross-references: EMBL:AL035356
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                     F;84-95/Region: FMN-phosphate binding #status predicted <FAD>
F;267-326,452-477/Domain: FAD binding #status predicted <FAD>
F;293-296/Region: FAD-pyrophosphate binding #status predicted
F;2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental
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N;Alternate names: NADPH-cytochrome P450 oxidoreductase
C;Species: Cavia porcellus (guinea pig)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
C;Accession: S27158; S38510
C;Accession: S27158; S38510
C;Accession: S1, Goda, T.; Ishizaki, K.; Kamataki, T.; Shinriki, N.
Biochim. Blophys. Acta 1171, 103-105, 1992
A;Title: Molecular cloning and sequence analysis of mouse NADPH-cytochrome P-450
A;Reference number: S27158; MUID:93041995; PMID:1420354
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                                                                                                                                                                                             Gaps
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                                                                                                                                                 14.1%; Score 767; DB 2; Length 677; 32.4%; Pred. No. 2.5e-35;
                                                                                                                                                                                             264;
                                                                                                        F;566/Binding site: NADP (Cys) #status experimental
                                                                                                                                                                                           Conservative 113; Mismatches
    F;82-224/Domain: flavodoxin homology <FLX>
                                                                                                                                                                     Similarity
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A; Residues: 1-678 <OHG>
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Matches 211;
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                                                                        444 FVVKAKSKKIP----LGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLYGSNMGTAEGTAR
                                                                                                                                                                                                                   DQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEG
                                                                                                                                                                                                                                                                                                                                                               -----GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNYEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 FLFRKKKEEIPEFTKISTTTSSVKESSFVEKMKKTGRN----IIVFYGSQTGTAEEFAN
                                                                                                                                              499 DLADIAMSKGFAPQVATLDSH----AGNLPR--EGAVLIVTASY-NGHPPDNAKQFVDWL
                                                                                                                                                                 157 QETDLD-LSGVKYAVFGLGNKTY-EHFNSMGKYVDQRLEQLGAQRIFELGLGDDDGNLEE
                                                                                                                                                                                                                                                                                                                         215 DFITWREQFWPAVCEFFGVEATGEESSIRQYELVL---HADTDPAKVYTGEMGRLKSYEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450 RLQARYYSIASSSKVHPNSVHICAVVVEYETKSGRIN-KGVATSWLQAKDPAGENGRRAL
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                                                                                                                                                                                                                                                                                           612 TYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMH-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT----
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                                    65;
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 Length
                                      Indels
Query Match 14.0%; Score 761.5; DB 2; Best Local Similarity 31.9%; Pred. No. 5e-35; Matches 208; Conservative 111; Mismatches 269;
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A; Experimental source: cultivar Columbia; BAC clone F22K18
R; Mignote-Vieux, C.; Kazmaler, M.; Lacroute, F.; Pompon, D.M.
submitted to the EMBL Data Library, May 1992
A; Reference number: $21530
A; Reference number: $21530
A; Molecule type: mRNA
A; Residues: 1-160,'S', 162-476,'CODW', 481-692 <MIG>
A; Coss-references: EMBL:X66016; NID:g16186; PIDN:CAA46814.1; PID:g16187
C; Genetics:
A; Gene: ATRI
A; Map position: 4
A; Introns: 101/3; 121/3; 147/2; 166/3; 194/3; 207/1; 230/2; 294/2; 325/2; 400/3; 428/3;
A; Note: F22X18 B.280
C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemopro
C; Keywords: flavoprotein; NADP; oxidoreductase
F; 85-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKD 1044
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                                                                                                                                                                                                                                                                                                                                                                                      103
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1 | |- | :|||||||||||| : :| :| | :| :| :|
455 PLGVFFAAIAPRLQPRYYSISSSPRLAPSRVHVTSALVYGPTPTG-RIHKGVCSTWWKNA
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A,Description: catalyzes the reduction of the heme-thiolate-dependent monooxygenases, A,Note: expression induced by fungal elicitor-treatment or or UV-irradiation C,Superfamily: NADPH-ferithemoprotein reductase; flavodoxin homology; NADPH-ferrihemo C;Keywords: flavoprotein; NADPP; oxidoreductase F;74-680,Domain: NADPH-ferrihemoprotein reductase homology <FEH>
                                                                                                                                                                  parsley
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - parsley
N.Alternate names: NADPH cytochrome P450 reductase
C.Species: Petroselinum crispum (parsley)
C.Species: Petroselinum crispum (parsley)
C.Date: 20.5ep-1999 #text_change 03-Jun-2002
C.Accession: T14903
R.Koopmann, E.; Hahlbrock, K.
Proc. Natl. Acad. Sci. U.S.A. 94, 14954-14959, 1997
A.Title: Differentially regulated NADPH:cytochrome P450 oxidoreductases in parsl
A.Reference number: Z18258; MUID:98070859; PMID:9405720
A.Reternce number: L18258; MUID:98070859; PMID:9405720
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-681 <KOO>
A.Cross references: EMBL:AF024634; NID:92809384; PIDN:AAB97736.1; PID:92809385
C.Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 VEEAEKLIGMOPNTYFSVHIDDEDGTPLTGGSLPPPFPPCTVRSALAKYADLLSSPKKSA
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Pred. No. 1.1e-33;
; Mismatches 275;
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30.7%;
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C;Function:
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C;Species: Salmo trutta (brown trout)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 03-Jun-2002
                                                                         NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - brown trout (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A47298
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - mung bean
N;Alternate names: NADPH-cytochrome P450 reductase
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                                                                                                                                                   Rikoener, J.F.; Carino, F.A.; Feyereisen, R.

Rikoener, J.F.; Carino, F.A.; Feyereisen, R.

Insect Biochem. Mol. Biol. 23, 439-447, 1993

A.Title: The CDNA and deduced protein sequence of house fly NADPH-cytochrome P450 reduct
A.Reference number: A56592; MUID:93284260; PMID:8508186
A.Accession: A56592
A.Status: preliminary
A.Moclecule type: DNA; mRNA
A.Residues: 1-671 < KOBS
A.Residues: 1-671 
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NyAlternate names: NADPH-cytochrome P450 reductase; P450 reductase c) Species: Musca domestica (house fly) c) Species: Musca domestica (house fly) c) Date: 11-Mug-1995 #sequence_revision 11-Aug-1995 #text_change 03-Jun-2002 C) Accession: A56592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|: | : |: || || || || || XEWITNGEVD-LTGLNYAVFGLGNKTY-EHYNKVAIYVDKRLEELGATRVFELGLGDDDA
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Circaesion: A28577
RiUrenjak, J.; Linder, D.; Lumper, L.
T. Chromatogr. 397, 123-136, 1987
A; Title: Structural comparison between the trout and mammalian hydrophilic domain of A; Reference number: A28577; MUID:88008061; PMID:3116019
A; Rolecule type: protein
A; Residues: 1-601 GNES
C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemocyseyords: flavoprotein; NADPH-ferrihemoprotein; reductase
F; 25-599/Domain: NADPH-ferrihemoprotein reductase
F; 27-169/Domain: flavodoxin homology <FLX>
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                                                                                                                                                                                                                                                                                                                                Length 601;
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Matches 195; Conservative 106; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                13.2%; Score 723; DB 2; 30.2%; Pred. No. 6.1e-33;
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us-10-031-146-2\_1.rpr

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R;Rosco, A.; Paullí, H.H.; Priesner, W.; Kutchan, T.M.
Arch. Biochem. Blophys. 348, 369-377, 1997
A;Title: Cloning and heterologous expression of NADPH-cytochrome P450 reductases from A;Reference number: 217096; MUID:98096363; PMID:9434750
A;Rocession: T10720
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-683 <R:S>
                                                                                                                                                                                                                                            A; Description: catalyzes the reduction of the heme-thiolate-dependent monooxygenases; C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo C; Keywords: flavoprotein; NADP; oxidoreductase F; 80-682/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F; 80-682/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
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                                                                                                                                                                                         A;Cross-references: EMBL:U67185; NID:g2580496; PIDN:AAC05021.1; PID:g2580497 C;Function:
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NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - spring vetch
C;Species: Vicia sativa (spring vetch, tare)
C;Date: 20-May-1994 #sequence_revision 03-Aug-1995 #text_change 03-Jun-2002
C;Accession: S37159
R;Benveniste, I.; Begue-Kirn, C.; Lesot, A.; Hasenfratz, M.; Durst, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 IDKEEEEIEVDPGKIKLTIFFGTQTGTAEGFAKALAEEIKAKYKKAVVKVVDLDDYAAED
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Best Local S
Matches 191
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             C; Accession:
R; Rosco, A.;
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C;Species: Vigna radiata (mung bean)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 03-Jun-2002
C;Accession: A47298
R;Shet, M.S.; Sathasivan, K.; Arlotto, M.A.; Mehdy, M.C.; Estabrook, R.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 2890-2884, 1993
A;Title: Purification, characterization, and cDNA cloning of an NADPH-cytochrome P450 re
A;Reference number: A47298; MUID:93219390; PMID:8464904
A;Accession: A47298; MUID:93219390; PMID:8464904
A;Accession: A47298; MUID:93219390; PMID:8464904
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-600 cSHE>
A;Experimental source: var. Berken, microsomes
A;Note: sequence extracted from NCBI backbone (NCBIP:128723)
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein; Reverence it lavoporotein; NADPH-ferrihemoprotein reductase
F;84-233/Domain: flavodoxin homology <FLX>
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N;Alternate names: ferrihemoprotein P-450 reductase; NADP-cytochrome reductase
C;Species: Papaver somniferum (opium poppy)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
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196 VYDEELAEQGAKRLVAVGLGDDDQSIEDDFSAWKESLWSELD-----QLLRDEDDANTVS
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CIHLEFDISGTSITYDTGDHVGVYAENCNETVEETGKLLGQNLDLFFSLHTDKDDGTSLG
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submitted to the EMBL Data Library, September 1993
A;Description: Isolation and characterization of a cDNA encoding an NADPH-cytochrome P45
A;Reference number: S37159
A;Accession: S37159
                                                                                                                                              A,Cross-references: EMBL:226252; NID:g400531; PIDN:CAA81211.1; PID:g400532
C.Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemopro
C;Keywords: flavoprotein; NADP; oxidoreductase
F;83-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
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                                                                                                                                                                                                                                                                                                                                                                                                                            466 SAKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLAD--IAMSKGFAPQVATLDSHA--- 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            894 PETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQ 953
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                             92;
                                                                                                                                                                                                                                                                 Query Match 13.0%; Score 711; DB 2; Length 69. Best Local Similarity 28.4%; Pred. No. 3.5e-32; Matches 198; Conservative 120; Mismatches 287; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1013 LMKSYADVHQVSEAD---ARLWLQQLEEKGRYAKDVW 1046
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A; Molecule type: mRNA
A; Residues: 1-692 <BEN>
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Search completed: May 29, 2003, 08:31:43 Job time : 52 secs

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 29, 2003, 08:22:51 ; Search time 26 Seconds (without alignments) 1671.815 Million cell updates/sec Run on:

US-10-031-146-2 5457 1 TIKEMPQPRTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 ; Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		Description	P14779 bacillus me		008336 bacillus su	P37040 mus musculu	P00388 rattus norv		P00389 oryctolagus				Q27597 drosophila				Q06518 rattus norv	Q9z0j4 mus musculu	P29476 rattus norv		O60591 homo sapien	_	O19132 oryctolagus						O61608 anopheles s		P29473 bos taurus	P70313 mus musculu	_		Q27571 drosophila
SUMMARIES		OI.	CPXB_BACME	CYPD_BACSU	CYPE_BACSU	NCPR_MOUSE	NCPR_RAT	NCPR_PIG	NCPR_RABIT	NCPR_HUMAN	NCPR_CAVPO	NCPR_MUSDO	NCPR_DROME	NCPR_SALTR	NCPR_PHAAU	NCPR_CATRO	NOS2_RAT	NOS1_MOUSE	NOS1_RAT	NOS1_HUMAN	NS2D_HUMAN	NOS2_MOUSE	NOS1_RABIT	NS2A_HUMAN	NOS2_CHICK	NOS2_CAVPO	NOS_RHOPR	NCPR_CANMA	NOS_ANOST	NOS3_HUMAN	NOS3_BOVIN	NOS3_MOUSE	NOS3_PIG	NCPR_CANTR	NOS_DROME
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ø	Query	Match	100.0	60.7	60.1	14.3	14.2	14.1	14.1	14.1	٠	13.5	13.3	13.2	13.2	12.9	12.5	12.4	12.4	12.4	•	12.2	12.1		٠	11.9	11.8	•	11.3	٠				10.8	10.3
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019114. oryctolagus P36587 schizosacch	Q9ubk8 homo sapien P16603 saccharomyc	P38038 escherichia	P38039 Irmidea sta P38039 salmonella	P57503 buchnera ap	Q62600 rattus norv	Q17574 caenorhabdi	048921 glycine max	023365 arabidopsis
NOS2_RABIT NCPR_SCHPO	MTRR_HUMAN NCPR_YEAST	CYSJ_ECOLI	CYSJ_SALTY	CYSJ_BUCAI	NOS3_RAT	MTRR_CAEEL	C972_SOYBN	C973_ARATH
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563	534.5	518.5	495.5	488.5	480.5	466.5	460	459.5
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### ALIGNMENTS

RESULT 1 CCPAB_BACME LAD DT C1-AP DT 01-AP RR
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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Pivotal role of water in the mechanism of P450BM-3.";
Biochemistry 40:13456-13465(2001).
-!-FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. CATALYSES
HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1,
OMEGA-2 AND OMEGA-3 POSITIONS, WITH OPTIMUM CHAIN LENGTHS OF 14-16
CARBONS (LAURIC, MYRISTIC, AND PALMITIC ACIDS). THE REDUCTASE
DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
                                                                                               oxidized flavoprotein + H(2)0.
COFACTOR: FAD AND FNN.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00371; FPNCR.
PRINTS; PR00371; FPNCR.
PROSITE; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Multifunctional enzyme; FMN; FAD; Flavoprotein; 3D-structure; NADP.
DOMAIN 1 471 CXTOCHROME P450.
DOMAIN 472 1048 NADPH-P-450 REDUCTASE.
BINDING 400 400 HEME.
                                                                       CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                 ferrocytochrome.
CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH
                                                                                                                                                                                                                                                                                                InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003097; FAL_binding.
InterPro; IPR001709; FPN_CYL_redctse.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00175; NAD_binding; 1. Pfam; PF00258; flavodoxin; 1. Pfam; PF00667; FAD_binding; 1.
                                                                                                                                                                                                                  EMBL; J04832; AAA87602.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB; 1JPZ; 09-NOV-01.
                                                                                                                                                                                                                           PIR; A34286; A34286.
PDB; 2HPD; 31-OCT-93.
PDB; 2BMH; 31-JUL-94.
PDB; 1FAG; 12-FEB-97.
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PDB; 1BVY; 23-FEB-99
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                                                                                                                                                                                                                                                                                                                                  Length 1048;
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                                                                                                                                                                                                                                                                                                      117650 MW; B55EB0DA599EAED5 CRC64;
                                                                                                                                                                                                                                                                                                                               Score 5457; DB 1;
Pred. No: 9e-298;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 1048; Conservative
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                                                     GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG
                                                                                   AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
                                                                                                                EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK
                                                                                                                                                                           QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-168;
MEDLINE-97453479; PubMed=9308178;
Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
Duesterhoeft A., Ehrlich S.D.;
Sequence of the Bacillus subtilis genome region in the vicinity of
the lev operon reveals two new extracytoplasmic function RNA
polymerase sigma factors SigV and Sig2.";
Microbiology 143:2939-2943(1997).
                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable bifunctional P-450 NADPH-P450 reductase 1 [Includes:
Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                  PRT; 1061 AA
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Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S. Bruschi C.V. Capdwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., R. Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., R. Huita R., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Robysshi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Medina N., Mellado R.P., Mizuno M., Messil D., Nakai S., Noback M., R., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Pohi T.W., Pohi T.W., Portetelle D., Porwollik S., Prescott A.M., R. Presecan E., Pulic P., Purnelle B., Ropoport G., Rey Bark S., R. Ragor T., Scanlan E., Schloetter R., Scoffone F., Racconi E., Takapashi H., Takemaru K., Sakluchi J., Sekowska A., Servoeter R., Scoffone F., Rackeuchi M., Tamakas I., Tanaka I., Tarahashi H., Takemaru K., Vasarotti A., Tanaka T., Terper F., Vasarotti A., Wanniers P., Wipat A., Yanamanoto H., Vannier F., Vasarotti A., Wannuncten B., Waltiska H.F., Zummench M., Vannier P., Vasarotti A., Yanamanoto H., Yanane K., Yasanotti A., Yananetein E., Wedler E., We
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ferrocytochrome.
--- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)0.
---- COFACTOR: Fab AND FWN (By similarity).
---- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane;
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Oxidoreductase; Monooxygenase; Electron transport; Me
Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOCHROME P450.
NADPH-P-450 REDUCTASE.
HEME (BY SIMILARITY).
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InterPro; IPR001099; FAD_binding.
InterPro; IPR001709; FNL_cyt_redectse.
InterPro; IPR00125; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00067; P450; I...
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Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00371; FPNCR.
PRINTS; PR00385; P450.
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1061 AA;
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Pfam; PF00175;
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Length 1061;

DB 1;

Score 3314;

60.78;

1026 QKAYQAVHGTGEQEAQNWLRHLQDTGMYAKDVWAG 1060

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SEGIITLHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATL 1013
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                                                                                                   QLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEA 184
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                                     5 MPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDE
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                                                                                                                                                                                                                                                                                                                                                                                                      596 NIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDI-ENSEDNKSTLSLQFVDSAADMP
           Gaps
         12;
         Indels
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Pred. No. 7.1e-178;
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         Mismatches
         Conservative 156;
59.58;
Similarity
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Best Local Simi
Matches 628;
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A Kunst F., Oggaswara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Buriss R., Bourslar L., Brans A., Braun M., Brighnell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Benizot F., Devine K.M., Dusterhoft A., Brilch S.D., Emmerson P.T.,
Chaser P., Goffeau A., Galightly E.J., Grands D.T.,
China S.Y., Claser P., Goffeau A., Galightly E.J., Grandi G.,
Chiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A. Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A. Joris B., Karamata D., Kasahara Y., Maruno M.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Media N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Perescott A.M.,
Presecan E., Pujic P., Purnelle B., Rose M., Sadale Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sekiguchi A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Taramakoshi A.
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-1- CORACTOR: FAD AND FMN (By similarity).
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 390:249-256(1997).
-!- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
                                                                               16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable bifunctional P-450:NADPH-P450 reductase 2 [Includes:
Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97453479; PubMed-9308178; Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J., Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J., Duesterhoeft A., Ehrlich S.D.; "Sequence of the Bacillus subtilis genome region in the vicinity of the lev operon reveals two new extracytoplasmic function RNA polymerase sigma factors SigV and SigZ."; Microbiology 143:2939-2943(1997).
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                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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CATALYTIC ACTIVITY: NADPH '+ 2 ferricytochrome
  1054 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98044033; PubMed-9384377;
                                                      (Rel. 40, Created)
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               Bacillus subtilis
                                                                                                                                                                                                                        CYPE OR CYP102A3.
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
                                                                                                                                                                                              (EC 1.6.2.4)
                                                      16-OCT-2001
CYPE_BACSU
008336;
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MEDLINE-94281246; PubMed-8011664;
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P37040;
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                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1054;
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                                                                                                                                                                                                                                       PROSITE; PS00086; CYTOCHROME_P450; 1. Oxidoreductase; Monooxygenase; Electron transport; Membrane; Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
                                                                                                                                                                                                                                                                                                     HEME (BY SIMILARITY).
fw; 705F8E27866Call0 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                           NADPH-P-450 REDUCTASE.
                                                                                                                                                                                                                                                                                                                                   Ouery Match 60.1%; Score 3281.5; DB 1; Best Local Similarity 58.5%; Pred. No. 4.6e-176; Matches 614; Conservative 173; Mismatches 254;
                                                                                                                                                                                                                                                                                  CYTOCHROME P450
                                                                                                            Subtilist; BG12299; cypE.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001307; FAD_bindding.
InterPro; IPR001209; FPM_cyt_redctse.
InterPro; IPR001206; FPW_cyt_redctse.
InterPro; IPR001243; Oxred_FAD/NAD(P).
Pfam; PF00067; P450; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00258; flavodoxin; 1.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                118675 MW;
                                                                                 U93874; AAB80867.1; -.
                                                                                          Z99117; CAB14658.1;
P14779; 1JPZ.
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                                                                                                                                                                                                                                                                                                                                                                                       IMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGII
                                                                                                                                                                 AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
                                                                                                                                                                                            DASQQIRLEAEEEKLAHLPLAKTVSVEELL-QYVELQDPVTRTQLRAMAAKTVCPPHKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKQASITVSVVSGEAWSGYĞEYKGIASNYLAELQEGDIITCFISTPQSEFTLPKDPETPL
                                                                                               NADP
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SIMILARITY: THE FWN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME BS REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
NCBL_TaxID=10090;
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-1- CATALITIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
reductase (EC 1.6.2.4) (CPR) (P450R)
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993 -GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047

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                                                                                                                                                                                                                                           PRINTS; PR00369; F<u>T</u>AVODOXÍN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
Membrane; Acetylation.
                                                                                                                                                                                                                                                                                                                ACETILATION (BY SIMILARITY).
FEMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 106; Mismatches 267; Indels
                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                                                                                        InterPro; IPR003097; FAD_binding.
InterPro; IPR0013097; FAD_binding.
InterPro; IPR001094; FPN_Cyt_redctse.
InterPro; IPR001226; Flavdoxin.
InterPro; IPR00133; Oxred_FAD_NAD(P).
Pfam; PP00175; NAD_binding; 1.
Pfam; PP00558; Flavdoxin; 1.
Pfam; PP00567; FAD_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     76912 MW;
                                                                    EMBL; D17571; BAA04496.1; -. HSSP; P00388; 1AMO.
                                                                                                SWISS-2DPAGE; P37040; MOUSE
                                                                                                                 MGD; MGI:97744; Por.
                                                                                                                                                                                                                                                                                                                               169
313
450
529
624
677 AA;
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SEQUENCE
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               677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.80 ANGSTROMS) OF MUTANTS.
MEDLINE-21369908; PubMed=11371558;
Hubbard P.A., Shen A.L., Paschke R., Kasper C.B., Kim J.-J.P.;
"NADPH-cytochrome 4450 oxidoreductase. Structural basis for hydride
                                                                                                                                                                                                                                                                                                                                                                                                 domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and electron transfer.";
J. Biol. Chem. 276:29163-29170(2001).

J. Biol. Chem. 276:29163-29170(2001).

TO CYTOCHON: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NATIO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.

-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
'Three-dimensional structure of NADPH-cytochrome P450 reductase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang M., Roberts D.L., Paschke R., Shea T.M., Masters B.S.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MUTAMEN H., Yabusaki Y., Ohkawa H.;
Murakami H., Yabusaki Y., Ohkawa H.;
"Expression of rat NADPH-cytochrome P-450 reductase cDNA in Saccharomyces cerevisiae.";
                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
1-JAPR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                           Porter T.D., Kasper C.B.;
"Coding nucleotide sequence of rat NADPH-cytochrome P-450 oxidoreductaes CDNA and identification of flavin-binding of Proc. Natl. Acad. Sci. U.S.A. 82:973-977(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prototype for FMN- and FAD-containing enzymes."; Proc. Natl. Acad. Sci. U.S.A. 94:8411-8416(1997).
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MEDLINE-97385116; Pubmed-9237990;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-85140278; PubMed=3919392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 29:9814-9818(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 413-677 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1 - COFACTOR: FAD AND FMN.
                                                                                                       STANDARD;
                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ferrocytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5:1-10(1986)
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                                                                                                       NCPR_RAT
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us-10-031-146-2\_1.rsp

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                                                                                                                                                                  LLPRLQARYYSIASSSKVHPNSVHICAVAVEYEAKSGRVN-KGVATSWLRAKEPAGENGG 504
                                                                                                                                                                                                                              -GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                     FGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQ
                                                                     ---ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLY
                                                                                                                                                                                                                                                        MEDLINE-87075664; PubMed-3098240; Vogel F., Lumper L.; Vogel F., Lumper L.; Vogel F., Lumper L.; Vogel F., Lumper L.; Complete structure of the hydrophilic domain in the porcine NADPH-cytochrome P-450 reductase."; Blochem. J. 236:811-878[1986].

-I. FUNCTION: THIS ENZYME IS EQUIRED FOR ELECTRON TRANSFER FROM NATA OCTYCCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- COFACTOR: FAD AND FMN.
-1- SUBCELULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADPH REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haniu M., Iyanagi T., Miller P., Lee T.D., Shively J.E.;
Complete amino acid sequence of NADPH-cytochrome P-450 reductase
from porcine hepatic microsomes.";
Biochemistry 25:7906-7911(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Amborn J., Preliss B., Stender B., Viale M., Repp R.Z., Lampert
Kroger M., Lumper L.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1987 (Rel. 04, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                           677
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PIR; A00403; RDPG04.
PIR; A25584; A25584.
HSSP; P16435; 1B1C.
InterPro; IPR003097; FAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-87101085; PubMed-3099837;
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ferrocytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scrofa (Pig)
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SEQUENCE.
                                                                                                                                                                                                                              993
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NCPR_PIG
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  and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 RLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDKSLVVFCMATYGEGDPTDNAQDFYDWL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          552 DQASADEVKGVRYSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASDD 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 QETDVD-LIGVKFAVFGLGNK----TYEHFNAMGKYVDQRLEQLGAQRIFELGLGDDDGN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 YENQKPPFDAKNPFLAAVTANRKLNQ-GTERHLMHLELDISDSKIRYESGDHVAVYPAND 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGIVNRVTARFG--LDASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLR 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 SALVNQIGEILGADLDVIMSLNNLDEESNKKHPFPCPTTYRTALTYYLDITNP-PRTNVL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLADIAMSKGFAPQVATLDSH----AGNLPR--EGAVLIVTASY-NGHPPDNAKQFVDWL 551
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ACETYLATION (BY SIMILARITY).

FWN (PYRINDINE PART) (BY SIMILARITY).

FAD (ADP PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 14.2%; Score 777.5; DB 1; Length 677; al Similarity 32.2%; Pred. No. 3e-36; 211; Conservative 111; Mismatches 263; Indels 71;
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  Usage by
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A957C40E7CEB8F81 CRC64;
  this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPM_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR0010246; Flavdoxin_like.
InterPro; IPR001433; Oxrad_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00558; flavdoxin; 1.
Pram; PR00567; FAD_binding; 1.
PRINTS; PR00567; FLA_binding; 1.
PRINTS; PR00571; FPNCR.
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                                                                                                                                                                                M58933; AAA41683.1; JOINED.
M58934; AAA41683.1; JOINED.
M58935; AAA41683.1; JOINED.
M58936; AAA41683.1; JOINED.
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76831 MW;
                                                                                          EMBL; M10068; AAA41064.1; -.
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AAA41683.1;
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PDB; 1JA0; 22-AUG-01.
PDB; 1JA1; 22-AUG-01.
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313
450
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624
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modified entities
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MOD_RES
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-+ Local'
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PDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : |: | | | | ::: :| DIVMSLNNLDEESNKRHPFPCPTIYRT-ALTYYLDIINPPRTNVLYELAQYASEPSEGEQ 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEE 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 KKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAMSKGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 PQVATLD----SHAGNLPR-EGAVLI-VTASY-NGHPPDNAKQFVDWLDQASADEVKGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASDDFEGTYEEWREHM
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                                                                                                                                                                                                                                                                                                                                                                                                              401 IGQQFALHEAT-----LVLGMMLKHFDFEDHTNY--ELDIKETLT--LKPEGFVVKAKS
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InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001205; Flavdoxin_like.
InterPro; IPR001225; Flavdoxin_like.
InterPro; IPR001433; Oxred FRD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00259; flavodoxin; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum; Membrane; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                               ACETYLATION (BY SIMILARITY).
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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                        LAQFHAKGALTRLSVAFSR--EQPQKVYVQHLLKRDKEHLWKLIHDGGAHIYICGDARNM 635
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-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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J. Biol. Chem. 257:5929-5938(1982).
-I- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NATIO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Black S.D., Coon M.J.; "Structural features of liver microsomal NADPH-cytochrome P-450 reductase. Hydrophobic domain, hydrophilic domain, and connecting
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Katagiri M., Murakami H., Yabusaki Y., Sugiyama T., Okamoto M., Yamano T., Ohkawa H., "Molecular clonding and sequence analysis of full-length cDNA for rabbit liver NADPH-cytochrome P-450 reductase mRNA."; J. Biochem. 100:945-954(1986).
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                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)
                                                                            1006 APAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                  ARDVQNTFCDIVAEQGPMEHAQAVDYVKKLMTKGRYSLDVWS 677
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InterPro; IPR001094; Plavdoxin_like.
InterPro; IPR001126; Flavodoxin_
InterPro; IPR001433; Oxred_FAD/NAD(P).
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InterPro; IPR001709; FPN_cyt_redo
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                                                                                                                                                                                                                      STANDARD;
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PIR; A05233; A05233.
HSSP; P16435; 1B1C.
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Euteleostom1;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
            01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR)
                                        POR OR CYPOR.
                                                                                                 SEQUENCE
    EQDGKKLIELLDQ-GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEK 1038
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RQGKEVGETLLYYGCRRAAEDYLYREELAGFQKDGTLSQLNVAFSREQAQ-KVYVQHLL
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                                                                  FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (ALBOSE PART) (BY SIMILARITY).
NADP (ALBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
W -> NY (IN REF. 2).
E -> N (IN REF. 2).
W, BIA163FAS3A5988B CRC64;
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Pfam; PF00258; flavodoxin; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum; Membrane; Acetylation.
                                                                                                                                                                            96;
                                                                                                                                                       Length 679;
                                                                                                                                                      14.1%; Score 769; DB 1; Length 67
ilarity 31.7%; Pred. No. 8.9e-36;
Conservative 111; Mismatches 250; Indels
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MEDLINE-99156068; PubMed-10048323;
Zhao Q., Modi S., Smith G., Paine M., McDonagh P.D., Wolf C.R.,
Tew D., Lian L.Y., Roberts G.C., Darlessen H.P.;
"Crystal structure of the FMN-binding domain of human cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME PASO IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
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-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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TISSUE-Liver;
MEDLINE-90105300; PubMed-2513880;
MEDLINE-90105300; PubMed-2513880;
MEDLINE MED. MED. Birkett D.J., Lee T.D., Shively J.E.;
"Structural and functional analysis of NADPH-cytochrome P-450 reductase from human liver: complete sequence of human enzyme NADPH-binding sites.";
Biochemistry 28:8639-8645(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Czerwinski M., Sahni M., Madan A., Parkinson A.;
"Polymorphism of human CYPOR: expression of new allele."
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in human HL-60 cell.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
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Protein Sci. 8:298-306(1999).
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MEDLINE-92198003; Pubmed-1550342;
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676 AA

PRT;

STANDARD;

NCPR\_HUMAN STANDARD P16435; Q16455; Q9H3M8;

NCPR\_HUMAN

A D

RESULT 8

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REDUCTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                          Endoplasmic reticulum;
                                                                                                                                                                                                                                        FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.1%; Score 767; DB 1; Length 676; 32.4%; Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 113; Mismatches 264; Indels
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F -> L (IN REF. 2 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 883EA13797020D70 CRC64;
                                                                                                                                                                        rotein; FMN; FAD; NADP; Endo
Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN REF.
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/FTId-VAR_004617.
R -> Q.
                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR_004618
          InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001204; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin.
Pfam; PF00175; NAD binding; 1.
Pfam; PF000175; NAD binding; 1.
Pfam; PF000578; flavdoxin; 1.
PRINTS; PR00369; FLAVDOXIN; PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NI
Membrane; Acetylation; Polymorphism; 3D-s:
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 InterPro; IPR003097; FAD_binding
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i - CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO ORIGINATE FROM MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FMN; FAD; NADP; Endoplasmic reticulum;
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ACETYLATION (BY SIMILARITY).
FWN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
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-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93385164; PubMed-8373812;
MEDLINE-97385164; PubMed-8373812;
Modylya S., Goda T., IShlazaki K., Kamataki T., Shinriki N.;
Biochim. Biophys. Acta 1174:313-313(1993).
-i- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NATO CYTOCHROWE 8450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEM OXYGENASE AND CYTOCHROME B5.
-i- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
                                    9/9
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cavia porcellus (Guinea pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

NCBI_TaxID=10141;
STRAIN-Hartley;
MEDLINE-93041955; PubMed-1420354;
OMGIVA S., Goda T., Ishizaki K., Kamataki T., Shinriki N.;
"Molecular cloning and sequence analysis of guinea-pig NADPH-cytochrome P-450 oxidoreductase.";
                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                     Z
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InterPro; IPR001709; FPN_CYt_redctse.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
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                                                                                                                                                                                                                                                                                      Created)
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HSSP; P00388; 1AMO.
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                                                                                             FLFRKKKEEIPEFTKISTTTSSVKESSFVEKMKKTGRN-----IIVFYGSQTGTAEEFAN
                                                                                                                  DLADIAMSKGFAPQVATLDSH----AGNLPR--EGAVLIVTASY-NGHPPDNAKQFVDWL
                                                                                                                                                            DQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEG
                                                                                                                                                                                 156 QETDLD-LSGVKYAVFGLGNKTY-EHFNSMGKYVDQRLEQLGAQRIFELGLGDDDGNLEE
                                                                                                                                                                                                                          214 DFITWREQFWPAVCEFFGVEATGEESSIRQYELVL---HADTDPAKVYTGEMGRLKSYEN
                                                                                                                                                                                                                                                 -----GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNYEGI
                                                                                                                                                                                                                                                             271 QKPPFDAKNPFLAAVTTNRKLNQ-GTERHLMHLELDISDSKIRYESGGHVAVYPANDSNL
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                                                                                                                                 TYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koener J.F., Carino F.A., Feyereisen R.; "The cDNA and deduced protein sequence of house fly NADPH-cytochrome P450 reductase.";
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pancrustacea; Hexapoda;
Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
ADP (ADP PART) (BY SIMILARITY).
4CA758F28EB84938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                       Indels
                                                    208; Conservative 111; Mismatches 269;
                               Score 761.5; DB 1
Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Arthrópoda, Mandibulata,
Insecta, Pterygota, Neoptera, Endopterygota,
Muscomorpha, Muscoidea, Musca, Musca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insect Biochem. Mol. Biol. 23:439-447(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
 NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Rutgers; TISSUE-Abdomen;
MEDLINE-93284260; PubMed-8508186;
           76650 MW;
                               14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domestica (House fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
          677 AA;
                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCPR_MUSDO
Q07994;
 NP_BIND
SEQUENCE
                                                                                              41
                                                                                                                                                                                                                                                                                                                                     692
                                                                                                                                                                                                                                                                                                                                                                               823
                                                                                                                    661
                                                                                                                                       96
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                                 Query Match
                                           Local
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ID NCPR_MUSDO
DT 01-0CT
DT 01-0CT
DE NADPH-
OC EUKARY
OC EUKARY
OC EUKARY
OC NUSCON
NC NCBL_I
RN NCON
RN (I]
RN SEQUEN
RX MEDLII
RA KOENE:
RT P450
                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVVKAKSKKIPLGG-----IPSPSTEQSA--KKVRKKAENAHNTPLLVLYGSNMGTAE 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KILVEKLGKLCDANLDTVFSLINTDTDSSKKHPFPCPTTYRTALTHYLEITAIPRTHILK 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MONORPPEDAKNPFLASVIVNRELHK-GGGRSCMHIELDIDGSKMRYDAGDHIAMYPIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMP-----LAKMH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GAFSTNVVASKELQQPGSARSTRHLEIELP-KEASYQEGDHLGVIPRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGIVNRV--TARFGLD-ASQQIRLEAEEEKLAHLP---------LAKTVSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTARDLADIAM --- SKGFA -- PQVATLDS -- HAGNLPREGAVLIVTASYNGHPPDNAKQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFER FROM NADP
                                                                                                                -1 COFACTOR: FAD AND FAN.
-1 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-1 DEVELOPMENTAL STRAGE: EXPRESSED THROUGHOUT DEVELOPMENT, WITH HIGH LEVELS BEFORE METAMORPHOSIS AND LOW LEVELS IN PUPAE.
-1 SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADPH REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                       IT CAN ALSO PROVIDE ELECTRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FMN (PYRIMIDINE PART) (BY SIMILARIT
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
A00A2C35DFD8D129 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                         CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
REQUIRED FOR ELECTRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 735.5; DB 1;
Pred. No. 6.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 6.6e-34;
                                               TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001225; Flavdoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
                       CYTOCHROME P450 IN MICROSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FAD_binding; 1.
THIS ENZYME IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00258; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L19897; AAA29295.1; -. HSSP; P00388; 1AMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%;
30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                   ferrocytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618
671 AA;
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199; Conserv
                                                                                                                                                                                                                                                                                                                        REDUCTASE
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SEQUENCE
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ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKY 807

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Adams W.D., Celniker S.E., Holf R.A, Evans C.A., Gocayne J.D.,
R.A. Adams W.D., Celniker S.E., Holf R.A,
R.A. Adams W.D., Celniker S.E., Holf R.A,
R.A. Gocayer S.C., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R.A. Gutton G.G., Wortman J.R., Yandradla M.D., Zhang Q., Chen L.X.,
R.A. Sutton G.G., Wortman J.R., Yandradla M.D., Zhang Q., Chen L.X.,
R.A. Brandon R.C., Ragers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
R.A. Ballew R.M., Basu A., Barman B.P., Bhardari D., Bolshakov S.,
R.A. Bernos P.V., Berman B.P., Brotter P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
R. Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Doubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
R. Posler C., Gabriellan A.E., Garg W.S., Gelbart W.M., Glasser K.,
R. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Heuck J.,
R. Harris N.L., Harvey D., Heiman T.J., Weinnison J.A., Ketchum K.A.,
R. Jalali M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,
R. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                           KLIELL-DOGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAK 1043
                                                                                      || :| | : || || : || ELAEY---GKEKYQNWIQNSSRNIVHILEDI 431
                                                                                                                                                   868 LAELQE--GDT-ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQG 924
                                                                                                                                                                                                                                     QSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNQPKTYVQHVMEQDGK 984
                                                                                                                                                                                                                                                                                                                                                               608 LIWKVIGEOKGHFYICGDAKNMAVDVRNILVKILSTKGNMNESDAVQYIKKMEAQKRYSA 667
                                                                                                                                                                                       MKEKNPSVGEVKVPVFIR--KSQFRLPTKSEIPIIMVGPGTGLAPFRGFIQERQFLRDGG
                                                             808 PACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
STRAIN-Canton-S; TISSUE-Antenna;
MEDLINE-973111413; PubMed-9168130;
Hovemann B.T., Sehlmeyer F, Malz J.;
"Drosophila melanogaster NADPH-cytochrome P450 oxidoreductase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCPR_DROME STANDARD; PRT; 679 AA. 027597; 09VMF2; C=0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 16-0CT-2001 (Rel. 40, Last annotation update) NADPH-CYLOChrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Berkeley;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 189:213-219(1997).
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RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Maray D.E.,

RA Mount S.M., Molson K., Nixon K., Misskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Falazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Siden Klamos I., Simpson M., Skrong R., Sun E.,

Spier E., Spradiing A.C., Stapleton M., Skrong R., Sun E.,

RA Spier E., Wassarman D.A., Wenles E., Wang A.H., Wang X.,

RA Shan S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Theory S. Zaveri J. S., Zhan M., Zhang G., Zhao Q., Zheng I.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O.,

RT "The genome sequence of Drosophila melanogaster.";

CI - FUNCTION: THIS ENIZME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP

TO CYTCCHROME 9450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON

TO CYTCCHROME 9450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON

TO CYTCCHROME 9450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON

TO CYTCCHROME 9450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON

TO CYTCCHROME 9450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON

CC CTACALRY THE OLEME OXYGENASE ROW CATCCHROME BS. MAY FUNCTION TO CALLERY THE OLIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2

C --- CANALTY ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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REMBL; AE003613; AAF52367.1;

REMS; P16435; 11B1C.

RISPERONO15623; Cpr.

RICEPPO; IPRO010709; FPA_Dinding.

RICEPPO; IPRO012094; Flavdoxin_like.

RICEPPO; IPRO01243; Oxred_FAD/NAD(P).

RICEPPO; IPRO01433; Oxred_FAD/NAD(P).

REMS; PFO0175; NAD_Dinding; 1.

REMS; PRO0363; Flavodoxin; 1.

REMS; PRO0363; FLAVODOXIN.

REMS; PRO03639; FLAVODOXIN.

REMS; PRO036371; FROR.

WOXIGOREGUCLASE; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 SPSTEQSAKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAMS---KGFA--PQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE EN MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION (BY SIMILARITY).
-I TISSUE SPECIFICITY: HIGH IN ANTENNAE.
-i- DEVELOPMENTAL STAGE: EMBRYOS AND ADULTS.
-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS, THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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FAD (ADP PART) (BY SIMILARITY).
FAD (FLAUIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
AA -> VT (IN REF. 1).
S -> T (IN REF. 1).
I -> T (IN REF. 1).
I -> T (IN REF. 1).
W. C6387C111A0EDB4A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76346 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ferrocytochrome.
-1- COFACTOR: FAD AND FMN.
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331
467
555
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679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
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NP_BIND
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STANDARD;
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NADP+ REDUCTASE,
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426
434
601 AA;
                                                                                                                                                                             Similarity
           REDUCTASE.
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Matches 195;
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P37116;
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NON_CONS
SEQUENCE
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EGGGEEVLIRQYRLLEQPDVQPDRIYTGETARLHSIQNQRPPFDAKNPFLAPIKVNRELH 297
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          TLDS--HAGNLPREGAVLIVTASYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDK
                       NWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDI
                                                                 ENSEDNKSTLSLQFVDSAADMP-----LAKMH------GAFSTNVVASKELQ
                                                                                                                                          QPGSARSTRHLEIELP-KEASYQEGDHLGVIPRNYEGIVNRVTARFGLDAS---QQIRLE
                                                                                                                                                                                      AEEEKLAHLP-------LAKTVSVEELLQYVELQDPVTRTQLRAMAAĶTV
                                                                                                                                                                                                    SPE------GKEKYQSWIQDACRNIVHILEDIKSCRPPIDHVCELLPRLQPRYYSIS
                                                                                                                                                                                                                                                                            SSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQ----EGDTITCFISTPQSEF
                                                                                                                                                                                                                                                                                         TLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEE
                                                                                                                                                                                                                                                                                                                                   LENAQSEGIITLHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQG-AHFYICGDGSQMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Urenjak J., Linder D., Lumper L.;
"Structural comparison between the trout and mammalian hydrophilic actuctural comparison between the trout and mammalian hydrophilic domain of NADPH-cytochrome P-450 reductase.";
J. Chromatogr. A 397:123-136(1987).
-!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NA TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
-!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: FAD AND FWN.
SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
EN MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FWN-BINDING DOMAIN IS RELATED TO BACTERIAL
FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmo trutta (Brown trout).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Protinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_TaxID=8032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)
                                                                                                                                                                                                                                                                                                                                                                                                             1008 AVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
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Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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LYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKL-IELLDQGAHFYICGD 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PAPSTOETSFIEKMKKTGRN----IVVFYGSQTGTGEEFANRLSKDAHRYGMGSMAADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D----SHAGNLPREGAVLIV--TASY-NGHPPDNAKQFVDWLDQASADEVKGVRYSVFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRYYSISSSPRYDEKQASITVSVVSGEAWSGYGEY -- KGIASNYLAELQEGDTITCFIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYQEELEQAHKKGALTKLNVAFSREQDQ-KVYVQHLLRKNKVDLWRQIHEDYAHIYICGD
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                                                                                                                                                                                                                                                            Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1002 GSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
Phaseolus aureus (Mung bean) (Vigna radiata).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 :::: | || || 556 ARNWARDVQTAFYEIAEELGGMTRTQATDYIKKLMTKGRYSQDVWS
                                                                                                                                                                                                                                                                                                                                                                                                                  BC801767DE1D44C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.2%; Score 723; DB 1; I 30.2%; Pred. No. 2.8e-33; tive 106; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDIENSEDNKSTLSLQFVDSAADMPLAKMH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 106; Mismatches
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                                                     PIR; A28577; A28577.
HSSP; P16435; 1B1C.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
PRINTS; PR00369; FLAVODOXIN.
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293 765

789 429 546

961

489 902

us-10-031-146-2\_1.rsp

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962 TAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVH 1021
                                                                                                                                                                                                                                                                                                           311 CIHLEFDISGTSITYDTGDHVGVYAENCNETVEETGKLLGQNLDLFFSLHTDKDDGTSLG
                                                                                                                                                                                      SKWVVGSQRSLVEVWAREFPSAKPPLGVFFAAIAPRLQPRYYSISSSPRFAPQRVHVTCAL
                                                                                                                                                                                                                                                           490 VYGPTPTG-RIHKGVCSTWMKNAIPSEKSODCSSAPIFIR--PSNFKLPVDHSIPIIMVG
                                                                                                                                                                                                                                                                                           PGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIIT-LH
                                              681 TRHLEIELP-KEASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEKLAHL-
                                                                                                         ----PLAKTVSVE-ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---KQAY
                                                                                                                                                                      790 KEQVLAKRLTMLELLEKYPACEMKFSEFI-ALLPSIRPRYYSISSSPRVDEKQASITVSV
                                                                                                                                                                                                                               VSGEAWSGYGEYKGIASNYL----AELQEGDTITCFISTPQSEFTLPKDPETPLIMVG
                                                                                                                                       GSLLPPFPGPCSLRTALARYADLLNPPRKAALLALATH-ASEPSDERLKFLSSPQGKDEY
                                                                                                                                                                                                                                                                                                                                                                                                                   1022 QVSEADARLWLQQLEEKGRYAKDVW 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94035173; PubMed-8220474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1 - COFACTOR: FAD AND FMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-cv. Morning mist,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vinceae; Catharanthus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                   Shet M.S., Sathasivan K., Arlotto M.A., Mehdy M.C., Estabrook R.W.;
"Purification, characterization, and cDNA cloning of an NADPH-cytochrome P450 reductase from mung bean.";
Proc. Natl. Acad. Sci. U.S.A. 90:2890-2894(1993).

-1. FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVLIVTASY - NGHPPDNAKQFVDWLDQASADE---VKGVRYSVFGCGDKNWATTYQKVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 LQFVDSAADM-----PLA----PLA-----KMHGAFSTNVVASKELQQPGSARS
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              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00369; FLAVODOXÍN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FWN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
NALINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                      SIMILARITY: THE FWN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION, PTM: GLYCOSYLATED.
                                                                                                                                                                                                              CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (P. 592966167E8561DE CRC64;
                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-cv. Berken; TISSUE-Seedling;
MEDLINE-93219390; PubMed-8464904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin.
InterPro; IPR001433; Oxred_FAD_NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FAD_binding; 1.
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Sukaryota; Viridiplantae;
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639
275
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690 AA;
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                                            NCBI_TaxID-3916;
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CARBOHYD
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roseus encoding NADPH:cytochrome P-450 reductase, an enzyme essential for reactions catalysed by cytochrome P-450 mono-oxygenases in
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SIMILARITY: THE EMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Sukaryota, Viridiplantae; Streptophyta, imbryophyta; Tracheophyta; Spermatophyta; eudicotyladons; core eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioldeae;
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TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER. TO HEME OXYGENIASE AND CYTOCHROME B5.
-i- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verpoorte R., Hoge J.H.C.; "Isolation ac CDNA clone from Catharanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meijer A.H., Lopes Cardoso M.I., Voskuilen J.T., de Waal A., Verpoorte R., Hoge J.H.C.;
                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
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                                                                                                                                                                                                                                                                       714 AA
| | | :::| || :||| 666 NVDSTKAEAIVKKLQMDGRYLRDVW 690
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InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FAD_binding.
InterPro; IPR001205; Flavodoxin_like.
InterPro; IPR001226; Flavodoxin_like.
InterPro; IPR001233; Oxred_FAD_NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00567; FAD_binding; 1.
Pfam; PF00567; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
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FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
DBDD9AF41374CF91 CRC64;
 NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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EMBL; X09417; CAA70571.1; -.
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HLYFGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIEL 989
                                     LDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVW 1046
                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-93221515; PubMed-7682072;
Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
Hepatocytes and macrophages express an identical cytokine inducible
nitric oxide synthase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karlsen A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J., Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B., Mandson T., Boel E., Nerup J.; "Cloning and expression of cytokine-inducible nitric oxide synthase Diabetes 44:753-758(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley; TISSUE=Astrocytes;
MEDLINE=49.231594; PubMed=7513765;
Galea E., Reis D.J., Feinstein D.L.;
"Cloning and expression of inducible nitric oxide synthase from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Vascular smooth muscle;

BEDLINE-93191721; Pubmed-7680561;

Nunokawa Y., Ishida N., Tanaka S.;

"Cloning of inducible nitric oxide synthase in rat vascular smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K., Kawasaki H., Sugimura T., Esumi H.; Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nirric-oxide synthase from rat liver and its expression in COS 1 cells.";
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                                                                                                                                                                                                                                                                                                                                                      NOS2_RAT STANDARD; PRT; 1147 AA. Q06518; D9774; 035765; 035766; 064558; 064005; 063267; 01-JUN-1994 (Rel. 29, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, inducible NOS) (1NOS).
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MEDLINE-95309542; PubMed-7540573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Neurosci. Res. 37:406-414(1994)
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MEDLINE-94039059; PubMed-7693462;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michel T., Balligand J.-L.;
Michel T., Balligand J.-L.;
"Isolation and characterization of INOS from rat cardiocytes.";
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN WITHBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXRETED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 426-788 FROM N.A. STRAIN-Dahl/Rapp salt sensitive strain; TISSUE-Vascular smooth muscle; MEDLINE-98195092; PubMed-9535415; Chen P.Y., Gladish R.D., Sanders P.W.; "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitric oxide + N NADP(+).
COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
SUBDINIT: HOMODIMER (BY SIMILARITY).
TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE MEDULLEY COLLECTING DUCT AND VASA RECTA BUNDLE.
INDUCTION: BY INTERPEREND GAMMA AND LIPOPOLYSACCHARIDE (LPS).
SIMILARITY: BELONGS TO THE NOS FAMILY.
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"cDNA cloning and expression of inducible nitric oxide synthase from
                                                                                                                                                                                                                                                                                                                       "Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and uterus.";
Biol. Pharm. Bull. 19:1374-1376(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Wistar, TISSUE-Renal glomerulus;
Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;
"Advances in the studies of NO synthesis regulation in mesanglial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location of an inducible nitric oxide synthase mRNA in the normal
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                                                                                                                                                                                                                                                        MEDLINE-97070590; PubMed-8913516;
Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
Futaki S., Niwa M.;
                                                                                                    Kosuga K., Yui Y., Hattori R., Sase K., Eizawa H., Aoyama Inoue R., Sasayama S.;
Iroue R., Sasayama S.;
Ironing of an inducible nitric oxide synthase from rat polymorphonuclear neutrophils.";
Endothelium 2:217-221(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley; TISSUE-Renal glomerulus; MEDLINE-94276509; PubMed-7516453;
                                        Biochim. Biophys. Acta 1218:421-424(1994).
                        muscle cells."
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                      smooth
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                                                                                  SEQUENCE FROM N.A.
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CALMODULIN-BINDING (POUTENTIAL).
FAM (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
ZINC (BY SIMILARITY).
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Conservative 114; Mismatches 236;
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InterPro; IPR004030; NO_synthase.
InterPro; IPR001433; Oxred_FAD/NAD(P).
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interpro; IPR001709; FPN_cyt_redctse.
interpro; IPR001094; Flavdoxin_like.
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                                                                        Pfam; PF00175; NAD_binding; 1. Pfam; PF00258; flavodoxin; 1.
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Pfam; PF02889; NO_Synthase; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
EMBL; D14051; BAA03138.1; -. EMBL; U26686; AAA85861.1; -.
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Oxidoreductase; NADP; FAD;
Zinc; Metal-binding; Multig
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048938 petroselinu 039036 arabidopsis 004434 pisum sativ Q9zhk0 rhodococcus Q9au07 populus bal Q9nkv3 bombyx mori

Q9r0w4 rattus norv Q09590 caenorhabdi Q9bdh6 equus cabal P91655 drosophila

048938 039036 004434 092HK0 09A007 09KW3 09KW3 09BDH6 P91655 09HG2 09HG2 09HG2 09HG2 09HG3 09HG3 09HG3 09HG3 09HG3 09HG3 09HG4 
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(without alignments)
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1 TIKEMPQPRTFGELKNLPLL......RLWLQQLEEKGRYAKDVWAG 1048
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Copyright (c) 1993 - 2003 Compugen Ltd.
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## RESULT 1 09Y8G7

01-NOV-1999 (TrEMBLrel. 12, Last sequence update).
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Bifunctional P-450:NADPH-P450 reductase protein (Fatty acid omega-hydroxylase) (P450foxy) [Includes: cytochrome P450 505 (EC 1.14.14.1);
NADPH-cytochrome P450 reductase (EC 1.6.2.4)]. PRT; 1066 AA. 01-NOV-1999 (TrEMBLrel. 12, Created) PRELIMINARY; Q9Y8G7

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium. NCBL\_TaxID=5507; Fusarium oxysporum.

STRAIN-MT-811;
MEDLINE-20564350; PubMed-10995755;
Kitazume T., Takaya N., Nakayama N., Shoun H.;
Kitazume T., Takaya N., Nakayama N., Shoun H.;
Fusarium oxysporum fatty-acid subterminal hydroxylase (CYP505) is
membrane-bound eukaryotic counterpart of Bacillus megaterium [1] SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION cytochrome P450BM3."; J. Biol. Chem. 275:39734-39740(2000) MEDIATE=6571003; PubMed=6830036; MEDIATE=6571003; PubMed=6830036; MEDIATE=65721003; PubMed=6830036; MEDIATE=65721003; PubMed=6830036; Makayama N., Takemea A., Shoun H.; Cytochrome P450foxy, a catalytically self-sufficient fatty acid hydroxylase of the fungus Fusarium oxysporum."; J. Blochem. 119:435-440(1996).

-I- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. SHOWS HIGHEST ACTIVITY TOWARD FATTY ACIDS WITH A CHAIN LENGTH OF 12-14 CARBONS. THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450. 8888888

FUNCTION, AND SUBCELLULAR LOCATION.

OXIDIZED FLAVOPROTEIN + H(2)0. -1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2 -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH

ALIGNMENTS

Q9p4e2 cunninghame Q968y4 physarum po Q9wtk6 cavia porce Q9tux8 canis famil

Q968Y4 Q9WTK6 Q9TUX8

991655 drosophila 994042 phanerochae 094048 rattus sp. 0940414 phanerochae 091414 phanerochae 091414 phanerochae 091410 mus musculu 09494 homo sapien 097604 canis famil 000141 aspergillus 094175 ovis aries 094176 bacillus ha 092174 bacillus su 092214 bacillus su

097604 Q00141 Q9C498 Q9N175 Q8XIW0 Q9K776 032214 Q96560

658.5

651.5

10

644.5 636.5 628.5 627.5 617.5 615.5

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

sp\_archea:\* sp\_bacteria:\*

SPIREMBL\_21:\*

Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Sal	Description	Q9y8g7 fusarium ox Q9hqe0 qibberella	Ografo streptomyce	Q60451 cricetulus Q40916 pseudotsuga	Q9sb48 arabidopsis Q48937 petroselinu					
* *	results protocolors to the softhe total	SUMMARIES	£	Q9Y8G7 09HGE0	Q9RD76	Q60451 Q40916	Q9SB48 Q48937	Q8VX49	039035	Q9AU08	Q9FVM7 Q9SUM3	024425
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762 776 822

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605 DSTLEKRGGTRLVPMGSADAATSDMFSDFEAWEDIVLWPGLKEKYKISDEESGGGKGLL- 663
                                                         PLNPKSTVARVFRRFSLAWDSFLKIQSEGP--TTLPTNVAISAFDVFSAYVELSQPATKR
                                                                                                                                                                       823 SIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFIS
                                                                                                                                                                                                                           883 TPQSEFTLPKDPE-TPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHE
                                                                                                                                                                                                                                                                                            896 ASSEAFHLPSDAEKTPIICVAAGTGLAPLRGFIQERAAMLAAGRTLAPALLFFGCRNPEI
                                                                                                                                                                                                                                                                                                                       DYLYQEELENAQSEGIITLHTAFSRMPNQPK - - TYVQHVMEQDGKKLIELLDQGAHFYIC
                                            644 LQFVDSAADMPLAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVI
                                                                                                  PRNYEGIVNRVTARFGLDASQQIRLEAEEEKLAHLPLAKTVSVEELLQ-YVELQDPVTRT
                                                                                                                                                        763 QLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=M-3125;
Proctor R.H., Seo J.-A., Plattner R.D.;
Characterization of four clustered and coregulated genes associated
"Characterization of four clustered and coregulated genes associated
With fumonish biosynthesis in Fusarium verticillioides.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
HSSP; P00388; 1392.
                                                                                                                                                                                                                                                                                                                                                                            1000 GDGSQMAPAVE----ATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVW 1046
                                                                                                                                                                                                                                                                                                                                                                                            | :: ||| : |||| | 1016 G-SREIGKAVEDVCVRLAIEKAQONGRDVTEEMARAWFERSRNE-RFATDVF 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pezizomycotina; Sordariomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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InterPro: IPR001094; FAD binding.
InterPro: IPR001094; Flavdoxin_like.
InterPro: IPR001026; Flavdoxin.
InterPro: IPR001709; FPN_Cyt_redctse.
InterPro: IPR001433; Oxred_FAD/NAD(F).
Pfam; PF00667; FAD binding; 1.
Pfam; PF00658; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizor
Hypocreales; Nectriaceae; Gibberella
NCBI_TaxID=117187;
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SEQUENCE 1115 AA; 123276 MW; 5C
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PF00067; p450; 1.
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PRINTS; PR00371; FPNCR.
PRINTS; PR00385; P450.
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            COFACTOR: BINDS ONE MOLE EACH OF FAD AND FWN (BY SIMILARIII). SUBCELLUIAR LOCATION: MEMBRANE-BOUND. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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407 407 HEME (BY SIMILARITY).
1066 AA; 117925 MW; 6B8123698C223DBA CRC64;
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                                                                   EMBL; AB030037; BAA82526.1;
HSSP; P14779; 1BVY.
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  FERROCYTOCHROME
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                                                     P450 FAMILY.
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1010 ELEAYETIGLVQVRRAYSRDPSAQDAQGCKYVTDRLGKCRDEVARLWMDGAQVLVCG-GK 1068
                                       QMAPAVEATLMKSYADVHQV-SEADARL---WLQQLEEKGRYAKDVW
                                                           17.6%;
41.9%;
                                                                                                                                                                                            01-MAY 2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Putative cytochrome P450. SCO0801 OR SCF43.12.
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                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                       Streptomyces coelicolor,
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Best Local S.
Matches 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFALHEATLVLGMALKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKK-----IPLGG 457
                                                                                        71
                                                                          QRLIKEACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKG
                                                                                                                                             115 YHAMWYDIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQ--PHP
                                                                                                                                                                                                              FITSMVRALDEAMNKLQRANPD-----DPAYDENKRQFQEDIKVMNDLVDKIIADRKA
                                                                                                                                                                                                                                                                                   SGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPH
                                                                                                                                                                                                                                                                                                                                                      VLOKAAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEY
                                                                                                                                                                                                                                                                                                                                                                                                                             346 PLEKGDELMVLIPQLHRDKTIWGDDVEEFRPERF--ENPSAIPQHAFKPFGNGQRACIGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 IPSPSTEQSAKKVRKKA------ENAHNTPLLVLYGSNMGTAEGTARDLADIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKGFAPQVATLDSHA-GNLPREGAVLIVTASYNGHPPDNAKQFVDWLDQASADEVKGVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|| : ::| :| | | |:::|| || ::|| || ERGFGIRAVDVVNNAIDRIPVGSPVILITASYNGEPADDAQEFVPWLKSLESGRLNGVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASD···--DFEGTYEEWRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HMWSDVAAYFNLD-----IENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVA-SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEEKLA-HLPLAKTVSVEELL-QYVELQDPVTRT-QLRAMAAKTVCPPH--KVELEALLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        846 VSVV------SGEAWS---GYG----EYKGIASNYLAELQEGDTITCFISTPQSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQG-QSLGEAHLYFGCRSPHEDYLYQE
                                                    2 IKEMPOPKTFGELKNLPLLNTDKPVOALMKIADELGEIFKFEAP-----GRVTRYL-SS
                       Gaps
                     113;
                       Indels
   Pred. No. 4.5e-83;
; Mismatches 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         = ::
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   33.78;
Best Local Similarity
Matches 380; Conserv
                                                                                                                     25
                                                                                                                                                                                                                                                                                                  192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERTINA 3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
Kinash H., Hopwood D.A.;
"A set of ordered coadhas and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycenes, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
PROSITE; PS00227; TUBULIN; 1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 527 AA; 57741 MW; 4A612C1B7A894780 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 417:141-147(2002).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AL136502; CAB66201.1; -.
                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 961; DB 16;
Pred. No. 4.3e-52;
80; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                               Saunders D.C., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
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527
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InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001217; Tubulin.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
                                                            Created)
   PRT;
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FVVKAKSKKIPLGG---IPSPSTEQSA--KKVRKKAENAHNTPLLVLYGSNMGTAEGTAR 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 LAQYASEPSEQEQLHKMASSSGEGKELYLSWVVEARRHILAILQDYPSLRPPIDHLCELL 437
                                                                                                                                                                                                                                                       146 QETDVD-LIGVKFAVFGLGNK----TYEHFNAMGKYVDQRLEQLGAQRIFELGLGDDDGN
                                                                                                                                                                                                                                                                                                                                261 QKPPFDAKNPFLAAVTTNRKLNQ-GTERHLMHLELDISDSKIRYESGDHVAVYPANDSTL
                                                                                                                                                     552 DQASADEVKGVRYSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASDD
                                                                                                                                                                                                                                                                                                        -----GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNYEGI
                                                                                                                                                                                                                                                                                                                                                                                                                        320 VNQIGEILGADLDVVMSLNNLDEESNKKHPFPCPTTYRT-ALTYYLDITNP-PRTNVLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          822 PSIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQ-G
                           FEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSL---OFVDSA----ADMPLAKMH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                768 AAKTVCPP-----HKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   877 -ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRRSDEDYLYREELARFHKDGALTQLNVAFSR-EQAHKVYVQHLLKRDREHLWKLIHEGG
                                                                             DLADIAMSKGFAPQVATLDSH----AGNLPR--EGAVLIVTASY-NGHPPDNAKQFVDWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudotsuga menziesii (Douglas-fir).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pseudotsuga.
NCBI_TaxID=3357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The molecular characterization of a set of cDNAs differentially expressed during Douglas-fir germination and early seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=[MIRB] FRANCO; TISSUE-SEEDLING;
Tranbarger T.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLrel. 01, Created)
01-OCT-2000 (TIEMBLrel. 15, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4).
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STRAIN-[MIRB] FRANCO; TISSUE-SEEDLING;
Tranbarger T.J., Misra S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Physiol. Plantarum 95:456-464(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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     144
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RLIKEACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGY 115
                                                                                                                                                                                                                                                   HAMMVDIAVQLVQKWERLNAD-EHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFI 174
                                                                                           202 TAMVGTLGYA----QRLNTVPAPLAPWLLRDASRRNAADIAHLNRTVDDLVRERRANGGT 257
                                                                                                                                                                                                                             ----SGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFL 280
                                                                                                                                                                                                                                                                                                    281 VKNPHVLQKAAEEAARVLVD-PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDT 339
                                                                                                                                                                                                                                                                                                                            340 VLGGEYPLEKGDELMVLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQ--HAFKPFGNGQ 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RACIGOGFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSMVRALDEAMNKLQRAN----PDDP-AYDENKRQFQEDIKVMNDLVDKIIADRKA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obdys S., Goda T., Hoshino T., Shinriki N., Kamataki T.;
"High-red yeast, construction of a novel strain of Saccharomyces
cerevislae stably exerting high activity of hamster cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TERMELTEI. 01, Last sequence update)
01-MAR-2002 (TERMELTEI. 20, Last annotation update)
NADPH-cytochrome P450 oxidoreductase.
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 19
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
EMBL: D81320; BAA11856.1; --
HSSP; P00388; IAMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         667 AA; 75850 MW; 2023F43DF4C1EF07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.2%; Score 773.5; DB 11; ilarity 32.1%; Pred. No. 3.9e-40; Conservative 117; Mismatches 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         667
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InterPro; IPR001206; Flavdoxin_like.
InterPro; IPR001206; Flavdoxin.
InterPro; IPR00143; Oxred_FAD_NAD(P).
Pfam; PF00567; FAD_binding; 1.
Pfam; PF00155; Flavdoxin; 1.
Pfam; PF00155; NAD_binding; 1.
PRINTS; PR00369; Flavdoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 APAPGRRTAAPGAADDAGDTVSAP 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 IPSPSTEQSAKKVRKKAENAHNTP 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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es 210; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=10029;
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26
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Q60451;
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VMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEE 1037
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                                                                                    651 KITEKGSYIWNLIAQGGYLYVCGDAKGMARDVHRTLHSIVQEQESVDSTSAEATVKKLQT 710
592 AIQKSGEKLGPAVLFFGCRNRQMDYIYEDELKSYVENGVLTELVLAFSR-EGATKEYVQH 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2020 (TrEMBLrel. 20, Last annotation update)
01-MAY-2020 (TrEMBLrel. 20, Last annotation update)
NADPH-FERRIHEMOPROTEIN reductase ATRI (EC 1.6.2.4).
F22K18.280 OR AT4G24520.
Arabidopsis thaliana (Mouse-ar cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.6%; Score 739.5; DB 10; Length 692; 29.6%; Pred. No. 5.7e-38; ive 120; Mismatches 257; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wambutt R., Mewes H.W., Lemcke K., to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wedler H., Wedler E., Wambutt R., Hoheisel J.,
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Mayer K.F.X., Schueller C.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequenoing project;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                               692 AA
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InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
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INTERPROJOSOF; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin_
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Best Local Similarity 29.6%; Pre
Matches 196; Conservative 120;
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PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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711 EGRYLRDVW 719
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Wedler H., Wedler E.,
Submitted (MAR-2000) t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEK-----LAHLPLAKTVSV 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 TGDHVGVYAENLSDTVEEAAKLLGYPLDTIISVHSDKEDGTPLGGSSLLPPFPGPCTLQT 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                     STRAIN-[MIRB] FRANCO; TISSUB-SEEDLING;
MEDLINE-21003320; PubMed-11117258;
Tranbarger T.J., Forward B.S., Misra S.;
"Regulation of NADPH-cytochrome P450 reductase expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 719;
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                                                                                                                                                                                                                                                                                     Tranbarger T.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 249767; CAA89837.3; -.
HSSP: P00388; 1AMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4AA9B1FBF5591A3D CRC64;
                                                                                                                                             Douglas-fir germination and seedling development."; Plant Mol. Biol. 44:141-153(2000).
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PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
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InterPro; IPR001709; FPN_Cyt_redctse.
InterPro; IPR002114; HPT_SerP_Site.
InterPro; IPR001433; Oxred_FAD_NAD(P).
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=[MIRB] FRANCO; TISSUE=SEEDLING;
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003097; FAD_binding
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                                                                               :: | : | : | | | | | : | : | SEBIKARYERAAVKVIDLDDYAADDDQYEEKLKKETLAFFCVATYGDGEPTDNAARFYKW
                                                                                                                                     LDQASADEVK -- GVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDD
                                                                                                                                                              AD--IAMSKGFAPQVATLDSHAGN-----LPRECAVLIVTASY-NGHPPDNAKQFVDW
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Aplales; Apiaceae; Petroselinum.
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MEDLINE-98070859; PubMed-9405720;
Koopmann E., Hahlbrock K.;
"Differentially regulated NADPH:cytochrome P450 oxidoreductases parsley.";
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Last annotation update)
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EMBL; AF024634; AAB97736.1; -.
HSSP; P00388; 1AMO.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence updi
01-MAR-2002 (TrEMBLrel. 20, Last annotation up
NADPH cytochrome P450 reductase (EC 1.6.2.4).
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InterPro; IPR001094; Flavdoxin_like.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cytochrome P450 reductase (EC 1.6.2.4).
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IPR001709; FPN_cyt_redctse. IPR001433; Oxred_FAD/NAD(P).
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                                      InterPro; IPR001433; Oxred_FaD/NU
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
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                                      Morant M., Hehn A., Werck-Reichhart D., Lesot A., Pallett K.;

"Exploration and Polymophism of the cytochrome P450 reductase family
of genes in wheat.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ30313, CAC633301.1;

InterPro; IPR001094; Flavdoxin_like.

InterPro; IPR001094; Flavdoxin_like.

InterPro; IPR0011709; FN cyt_redctse.

InterPro; IPR0011709; FN cyt_redctse.

Pfam; PF00567; FAD_binding; 1.

Pfam; PF0058; Flavdoxin; 1.

Pfam; PF00175; NAD_binding; 1.
                                                                                                                                                                                                                                                    Gaps
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Matches 198; Conservative 115; Mismatches 273; Indels
                                                                                                                                                                                                       703 AA; 77429 MW; 2FCA33AA106E1B36 CRC64;
                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                           Score 734.5; DB 1
Pred. No. 1.2e-37;
                                                                                                                                                                                                                            13.5%;
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PRINTS; PR00371; FPNCR.
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| 122 almalaahatdpteadrlrhlaspagkdeyaqllvanqrsllevmaefpsakpplgvffa 481
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                                                                                                                                                                                                                                                                                                                               A RO D.-K., Douglas C.;

"Functional characterization of cytochrome P450 reductase from the "Functional characterization of cytochrome P450 reductase from the "Functional characterization of cytochrome P450 reductase from the submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF302498; AAK15261.1; -...

R HSSP; P00388; IAMO.

R InterPro; IPR0013097; FAD_binding.

InterPro; IPR001226; Flavodoxin_like.

InterPro; IPR001226; Flavodoxin_like.

InterPro; IPR00133; Oxred-EAD/NND(P).

R Pfam; PF00667; FAD_binding; 1.

R Pfam; PF00155; NAD_binding; 1.

R Pfam; PF00155; NAD_binding; 1.

R Pfam; PF00175; NAD_binding; 1.

R Pfam; PF00175; PR00301; FPNCR.
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           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TREMBLrel. 17, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
NADPH-Cytochrome P450 oxydoreductase isoform 3.
Populus balsamifera subsp. trichocarpa x Populus deltoides.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.
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1.5e-36;
ches 275;
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PRELIMINARY;
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Ro D.-K., Douglas C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                           994 AHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVW 1046
                                                                                                     tch 13.1%; Score 714.5; DB 10; Length 692; al Similarity 29.2%; Pred. No. 2.1e-36; 193; Conservative 119; Mismatches 261; Indels 89;
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STRAIN-HEYNH, TISSUE-SEEDLING;
And offer-vieux C., Kazmaier M., Lacroute F., Pompon D.M.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; K6016, CAA46814.1;
EMBL; K6016, CAA46814.1;
RISP; P00388; JAWO.
RISP; P00388; JAWO.
RITERPRO; IPR001309; FAD_binding.
InterPro; IPR001226; Flavodoxin.
RITERPRO; IPR0017094; FNA_CAL_redctse.
RITERPRO; IPR001173; FNA_CAL_redctse.
RITERPRO; IPR001433; Oxred_FAD/NAD(P).
REPRO; PR00173; NAD_binding; 1.
Pfam; PF00057; RAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
Pram; PF00175; NAD_binding; 1.
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01, Last sequence update)
20, Last annotation update)
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PRINTS; PR00371; FPNCR.
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01-MAR-2002
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KLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKD 1044
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813 KFSEFI-ALLPSIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL--- 868
                                                               PLGVFFAAIAPRLQPRYYSISSCQDWAPSRVHVTSALVYGPTPTG-RIHKGVCSTWMKNA 513
                                                                                                                                                                                                                                                                   926 SLGEAHLYFGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGK 984
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                                                                                                                                                                      ---AELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQ
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R Rosco A., Paull H.H., Priesner W., Kutchan T.M.;

T Cloning and heterologous expression of NADPH-cytochrome P450

I Arch. Blochem. Blophys. 348:369-377(1997).

R HSSP, P00388; IAMO.

R InterPro; IPR001094; Flavdoxin_like.

R InterPro; IPR001094; Flavdoxin_like.

R InterPro; IPR001265; Flavdoxin_like.

R InterPro; IPR001265; Flavdoxin_like.

R InterPro; IPR00143; Oxred_FAD/NAD(P).

R Pfam; PF00658; flavdoxin: 1.

R Pfam; PF00658; flavdoxin: 1.

R Pfam; PF00175; NAD_binding; 1.

R Pfam; PF00175; NAD_binding; 1.

R Pfam; PF00175; PR000119; FNCR.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 20, Last annotation update)
NADPH:ferrihemoprotein oxidoreductase (EC 1.6.2.4).
Papaver somniferum (Opium poppy).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales; NCBI_TaxID=3469;
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326 747 368 786 428 845 488

694

211

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960 -LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYA 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=VAR. LOLITA, TISSUE-SEEDLING;
Benveniste I., Begue-Kirn C., Lesot A., Hasenfratz M., Durst F.;
"Isolation and characterization of a cDNA encoding an NADPH-cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---------ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---R
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                                                                                                     541 PDNAKQFVDWLDQASADEV--KGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIA
                                                                                                                                                                                                                                                                                                                                                    267 DPSIISVEDKFSNLANGNVSFDIHHPCRVNVAVQKELHKAESDRSCIHLEFDITGTGITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 AIGSSLPPPFPGPCTLHTALACYADLLSPPKKAALLALAAHASEPSEADRLKFLSSPQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 787 QAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-ALLPSIRPRYYSISSSPRVDEKQASIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vicia sativa (Spring vetch) (Tare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
                                                  GTAEGFAKALAEEVKARYEKAAVKVFDLDDYAMEDDQYEEKLKKETLALFMVATYGDGEP
                                                                                                                                                                                                     DRGEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLA--
                                                                                                                                                                                                                                                                                                       ------KMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEA-SY
                                                                                                                                                                                                                                                                                                                                                                                                          695 QEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEKLAHLPLAKTVSVE----
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Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
EMBL: 226522; CA881211.1;
HSSP: P00388; 1.922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TIEMBLrel. 01, Created)
01-NOV-1996 (TIEMBLrel. 01, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
NADPH-ferrihemoprotein reductase (EC 1.6.2.4).
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InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                       EEKLAHLPLAKTVSV-----EELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEA 782
                                                                                                                                                                                                                                                                                                    897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGI 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    595 ISELVIAFSR-EGEKKEYVOHKMMEKATDVWNVISGDGYLYVCGDAKGMARDVHRTLHTI 653
:| : | : | : | : | : | 301
APSVATPYIATVPEYRVVIHETTVAALDDKHINTANGDVAFDILHPC-RTIVAQQRELHK 301
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                                                                                                     : | :: | | :: | DGS----PQGSSLPPFFFGPCTLRSALARYADLLNPPRKASLIALSAHASVPSEAERLRF
                                                                                                                                                                                                                                                                          L---LEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-ALLPSIRPRYSISSSPRVD
                                                                                                                                                                                                                                                                                                                                                                            EKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDT-ITCFISTPQSEFTLPKDPETP
                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last anotation update)
01-JUN-2002 (TrEMBLrel. 21, Last anotation update)
NADPH-cytochrome P450 oxydoreductase isoform 1.
Populus balsamifera subsp. trichocarpa x Populus deltoides.
Eukaryotts, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Malpighiales; Salicaceae; Populus.
                                                                          PGSARSTRHLEIELP-KEASYQEGDHLGVIPRNYEGIVNRVTARFG--LDASQQIRLEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ro D.-K., Douglas C.; "Functional characterization of cytochrome P450 reductase from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.0%; Score 711.5; DB 10; Length 692; ilarity 28.9%; Pred. No. 3.3e-36; Conservative 110; Mismatches 252; Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76725 MW; 7AA8CC78B3C984D9 CRC64;
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR0011266; Flavdoxin.
InterPro; IPR0011269; FPN_cyt_redctse.
InterPro; IPR001109; FPN_cyt_redctse.
InterPro; IPR001433; Oxred FAD/NAD(P).
Pfam; PF001667; FAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00171; FPNCR.
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                                                                                                                                                                                                                                          SAKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLAD--IAMSKGFAPQVATLDSHA---
                                                                                                                                                                                                     -----DRGKTKVTVFYGTQTGTAEGFAKALAEEIKARYEKAVVKVVDMDDYAIDD
                                                                                                                                                                                                                                                                                       CA'-EHFNKIGKIVDEDL/TEQGAKRLVPVGLGDDDQSIEDDFNAWKETLMPELD-----QL
                                                                                                                                                                                                                                                                                                                        ---- KMHGAFSTNVVAS
                                                                                                                                                                                                                                                                                                                                                                     KELQQPGSARSTRHLEIELP-KEASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRL
                                                                                                                                                                                                                                                                                                                                                                                     :|| :| | || || :| :| :| :| :| || :| || :| || SELHKPQSDRSCIHLEFDLSGTGVTYETGDHVGVYAENCDETVEEAGKLLGQSLDLLFSL
                                                                                                                                                                                                                                                                                                                                                                                                                   EAEEEKLAHL-----PLAKTVSVEELLQ-YVELQDPVTRTQLRAMAAKTVCPPHKVELE
                                                                                                                                                                                                                                                                                                                                                                                                                                   DEKQASITVSVVSGEAWSGYGEYKGIASNYLAEL----QEGDTITCFISTPQSEFTLPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 APQRVHVTCALVEGPTPTG-RIHKGVCSTWMKSATPLEKSHDCSRAPIFIRPSNFKLPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              894 PETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            954 SEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEAT
                                                                                                                                 106 ALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQ
                                                                                                                                               ----GNLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQASADE---VKGVRYSVFGCGDK
                                                                                                                                                                                                                                                                          NWATTYQKVPAFIDETLAAKGAENİADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALLE----KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-ALLPSIRPRYYSISSSPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum (Wheat).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                           92;
                                                                                 Length 692;
                                                                                                           Indels
                                                           49CB4AEC8611BE99 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                 13.0%; Score 711; DB 10; 28.4%; Pred. No. 3.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | | | | | :::|: | | | :|| | L---HIVQQQENADSSKAEATVKKLQMDGRYLRDVW
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01-WAR-2002 (TrEMBLrel. 20, Last annotation
NADPH-cytochrome P450 reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 AA
                                                                                                      Conservative 120; Mismatches
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Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                           692 AA; 76912 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                             Oxidoreductase
                                                                                           Best Local Similarity
Matches 198; Conserv
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                                                          SEQUENCE
                                                                                   Query Match
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MEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEK 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 EKEVWLKDFNYAVFGLGNRQY-EHFNKVAKEVDELLLEQGGNRLVPCGLGDDDQCIEDDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 TAWKELVWPELDQLLRDEDDTTGATTPYTAAIPEYRVVFIDKSD------LEFEDKS--
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                                                    Ξ.
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                                                    Schaller
                                                                                             "Increasing expression of P450 and P450-reductase proteins from monocots in heterologous systems.";
Arch. Biochem. Biophys. 379:161-169(2000).
EMBL; AF123610; AAG17471.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 656;
                                                    Batard Y., Hehn A., Nedelkina S., Schalk M., Pallett K.,
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13.0%; Score 710; DB 10;
Best Local Similarity 29.5%; Pred. No. 3:7e-36;
Matches 197; Conservative 109; Mismatches 264;
                                                                                                                                                                                                                                 InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001205; Flavdoxin_like.
InterPro; IPR001709; FPN_CYL_redctse.
InterPro; IPR001403; Oxred_FAD/NAD(P).
Pfam; PF00568; Flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
STRAIN-CV. DARIUS;
MEDLINE-20322901; PubMed-10864454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00369; FLAVODOXIN
PRINTS; PR00371; FPNCR.
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                                                                             Werck-Reichhart D.
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SEQUENCE
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977 HVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLE 1036
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                                                                                                                                                                                                                                                                                        |: |||:||: | |: :: :346 YETGDHVGVLCDNLSETVDEALRLLDMSPDTYFSLHAEKED--GTPISSSLPPPFPPCNL 403
                                                                                                                                                                                                                                                                                                                                                                                                    464 VMAEFPSAKPPLGVFFAGVAPRLQPRFYSISSSPKIAETRIHVTCALVYEKMPTG-RIHK 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              862 GIASNYLAELQEGDTITCFISTP----QSEFTLPKDPETPLIMVGPGTGVAPFRGFVQAR 917
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                                                                                                                                                                               -EELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE----KQAYKEQVLAKRLTMLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLEKYPACEMKFSEFIA-LLPSIRPRYYSISSPRVDEKQASITVSVVSGEAWSGYGEYK
                                                                              236 LGDDDQCIEDDFTAWREALWPELDTILREEGDTAVATPYTAAVLEYRVSIHDSEDAKFN-
                                                                                                                                                                                                                                                       694 YQEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEKLAHLPLAKTVSV----
                                602 EADASDDFEGTYEEWREHMWSDV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bevan M., Kalicki J., Wohldmann P., Smith A., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                F9N11.60 OR AT4G330210.
Arabidopsis thaliana (Mouse-car cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SOUTHWICK A., Karlin Neumann G., Nguyen M., Lam B., Miranda M.,
Southwick A., Farlin Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Theologis A., Ecker J., Davis R.W.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL109796; CABS2465.1;
EMBL; AL109796; CABS1014.1;
EMBL; AF325101; AAK17169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Smith A., Mewes H.W., Lemcke K., Malicki J., Wohldmann P., Smith A., Mewes H.W., Lemcke K., Mayer K.F., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264; Indels
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NADPH-FERRIHEMOPROTEIN reductase (ATR2) (EC 1.6.2.4).
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InterPro: IPR001433; Oxred_FAD/NAD(P)
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
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InterPro; IPR001226; Flavodoxin.
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                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
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PRINTS; PR00371; FPNCR.
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GRYLRDVW 656
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Best Local S
Matches 190
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